

(19) World Intellectual Property Organization
International Bureau



(43) International Publication Date
4 January 2001 (04.01.2001)

PCT

(10) International Publication Number
WO 01/00846 A2

(51) International Patent Classification⁷: C12N 15/52,
15/54, 15/55, 15/61, 9/10, 9/18, 9/90, 1/21, C12P 7/64,
C07K 16/40

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(21) International Application Number: PCT/US00/18149

(22) International Filing Date: 30 June 2000 (30.06.2000)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:
60/141,798 30 June 1999 (30.06.1999) US
09/561,077 28 April 2000 (28.04.2000) US

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(81) Designated States (*national*): CA, JP.

(84) Designated States (*regional*): European patent (AT, BE,
CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC,
NL, PT, SE).

Published:

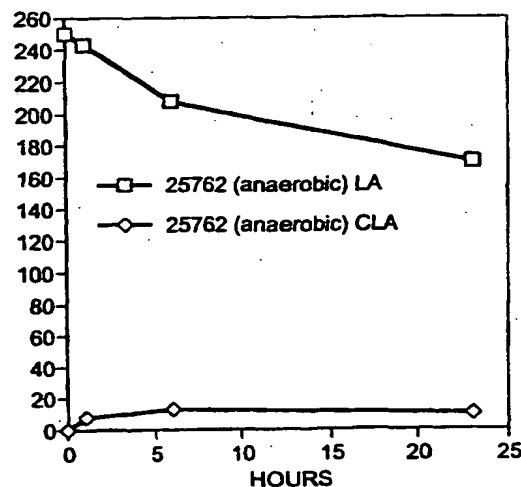
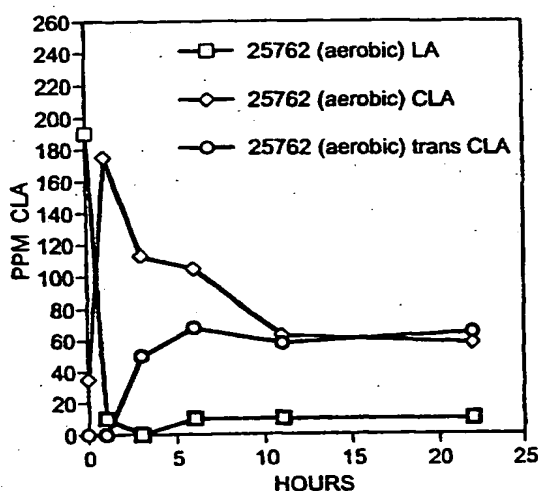
— Without international search report and to be republished
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For two-letter codes and other abbreviations, refer to the "Guid-
ance Notes on Codes and Abbreviations" appearing at the begin-
ning of each regular issue of the PCT Gazette.

(54) Title: LINOLEATE ISOMERASE



(57) Abstract: The present invention provides an isolated linoleate isomerase and its nucleic acid and amino acid sequences. The present invention also provides a method for producing conjugated linoleic acid or conjugated linolenic acid (CLA), or derivatives thereof, from an oil using an immobilized cell and/or an isolated linoleate isomerase. The present invention also provides an isolated lipase-like protein and its nucleic acid and amino acid sequences. The present invention also provides an isolated acetyltransferase-like enzyme and its nucleic acid and amino acid sequences.

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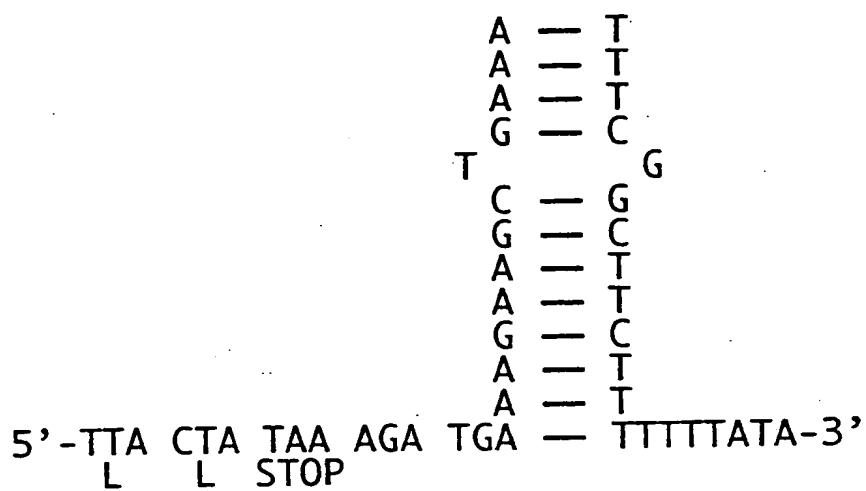
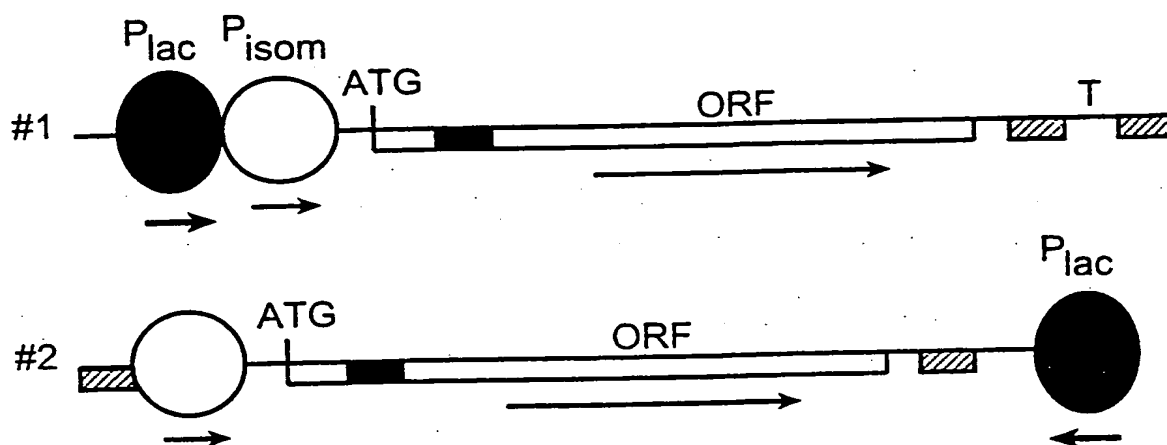


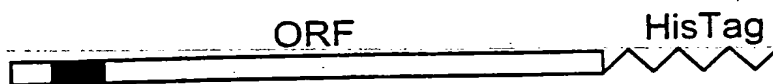
FIG. 10

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Tested Two Constructs



New Construct #3:



New Construct #4:



FIG. 11

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Expression System:

HapII promoter

LAT promoter

— with the secretion signal peptide

— without the secretion signal peptide

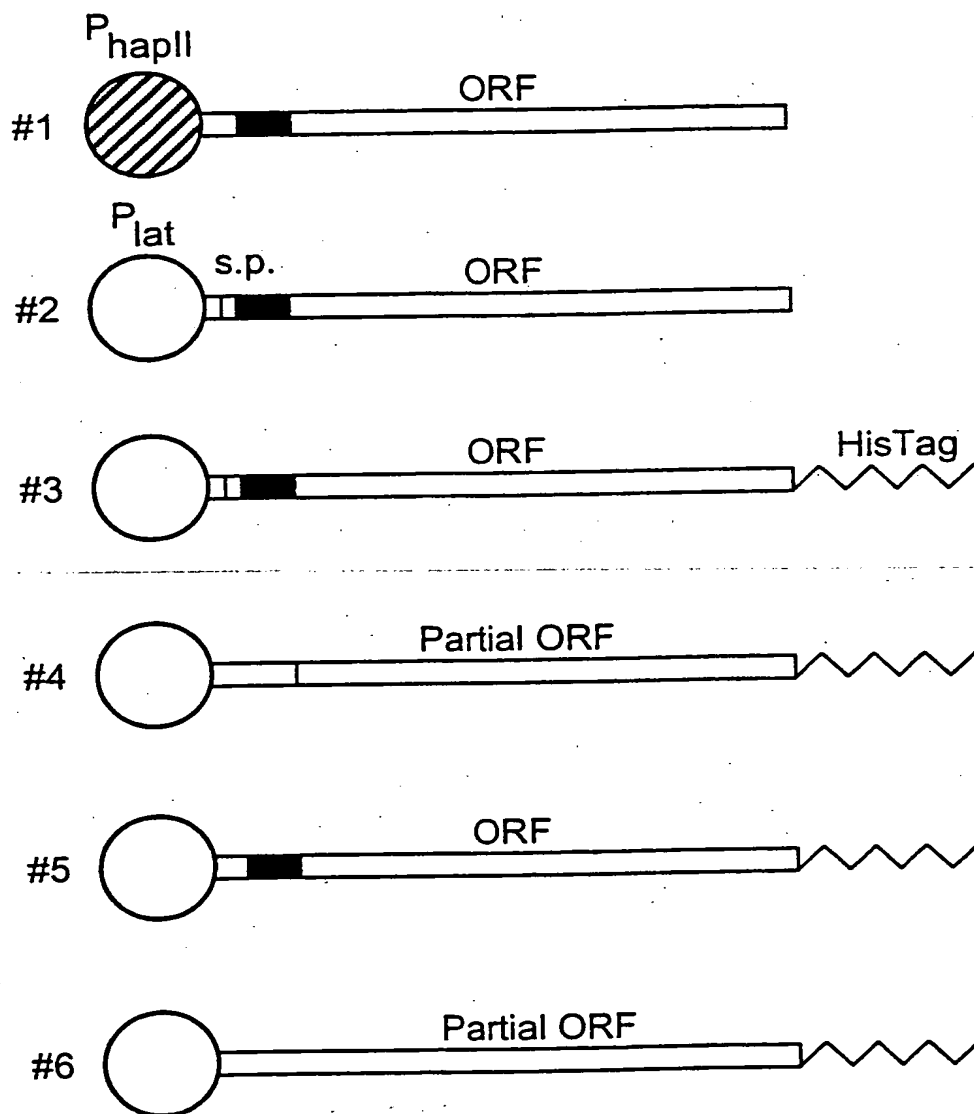


FIG.12

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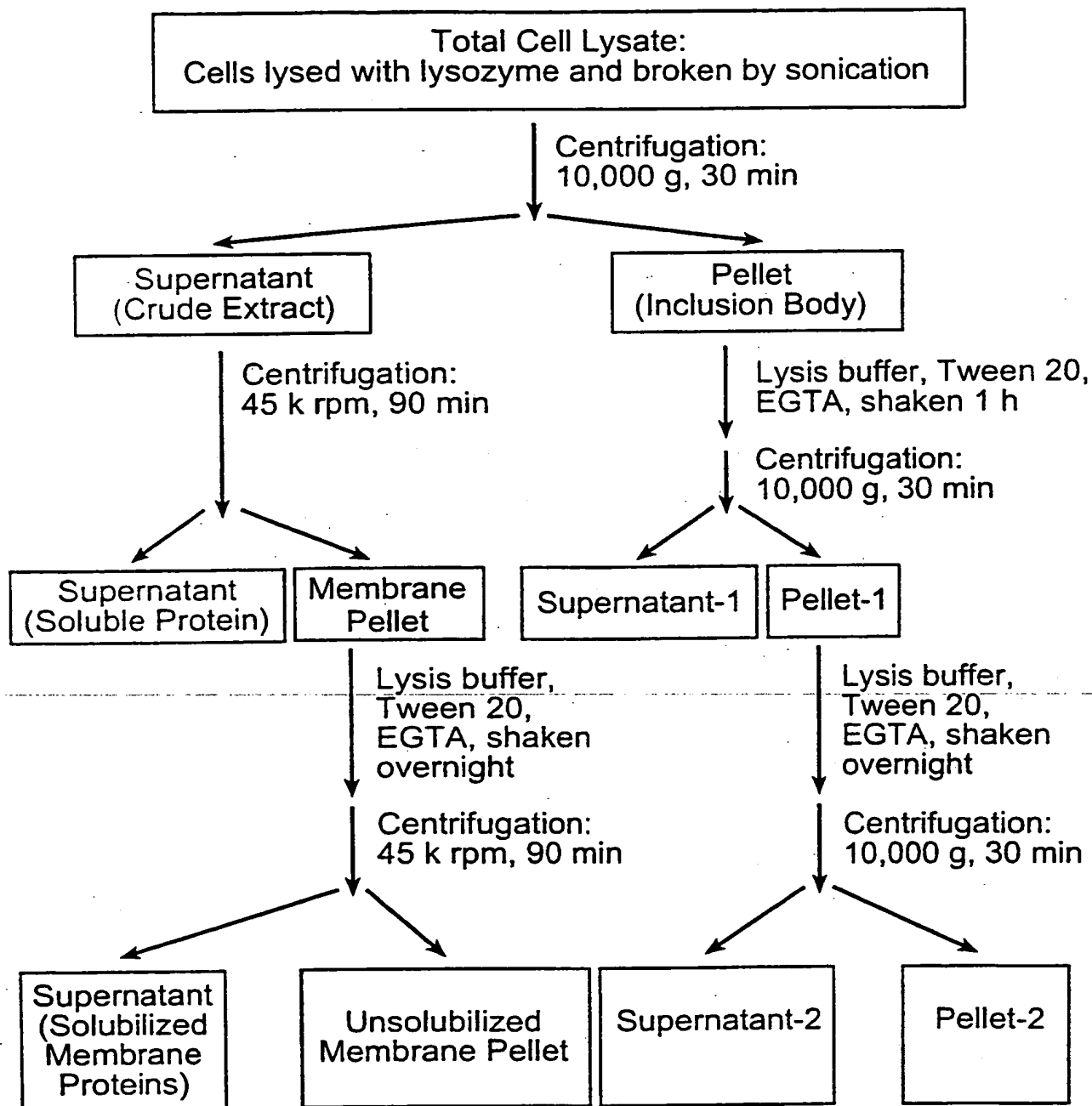


FIG. 13

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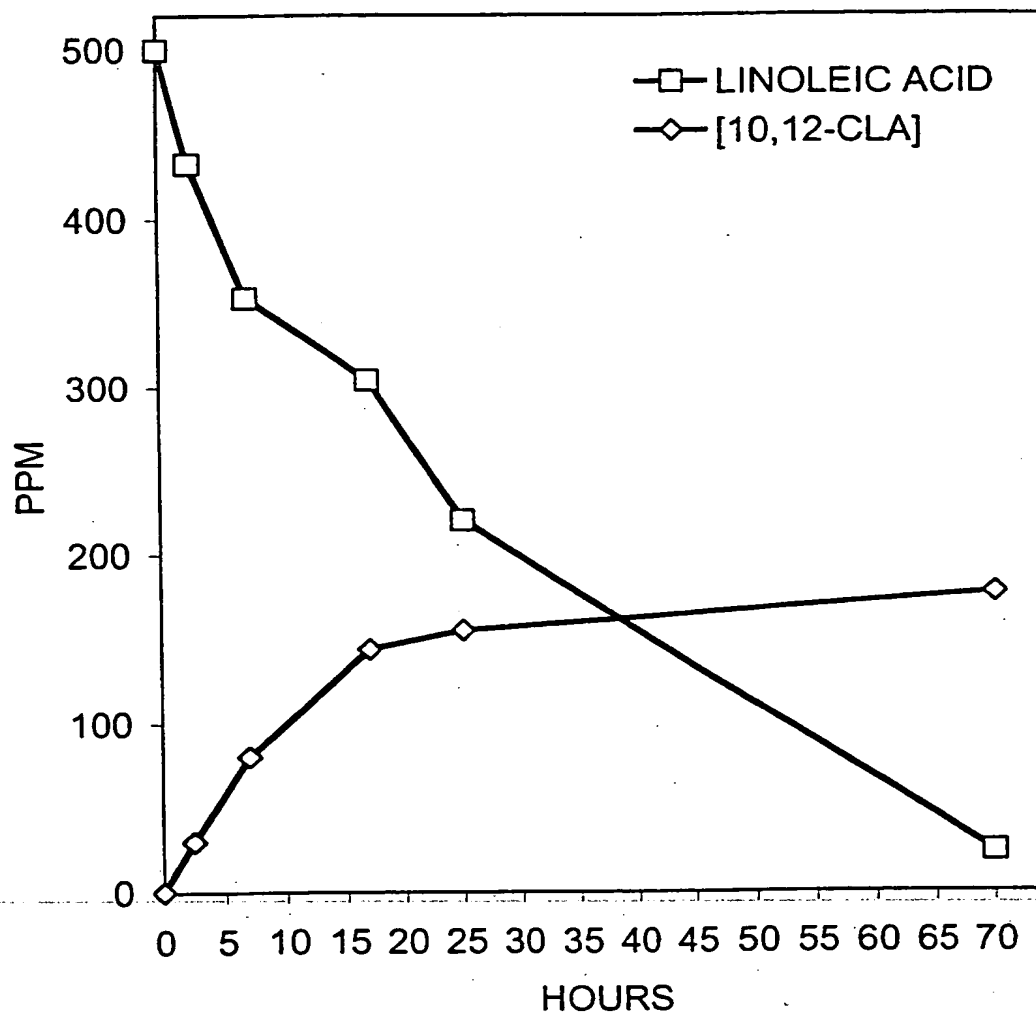


FIG. 14

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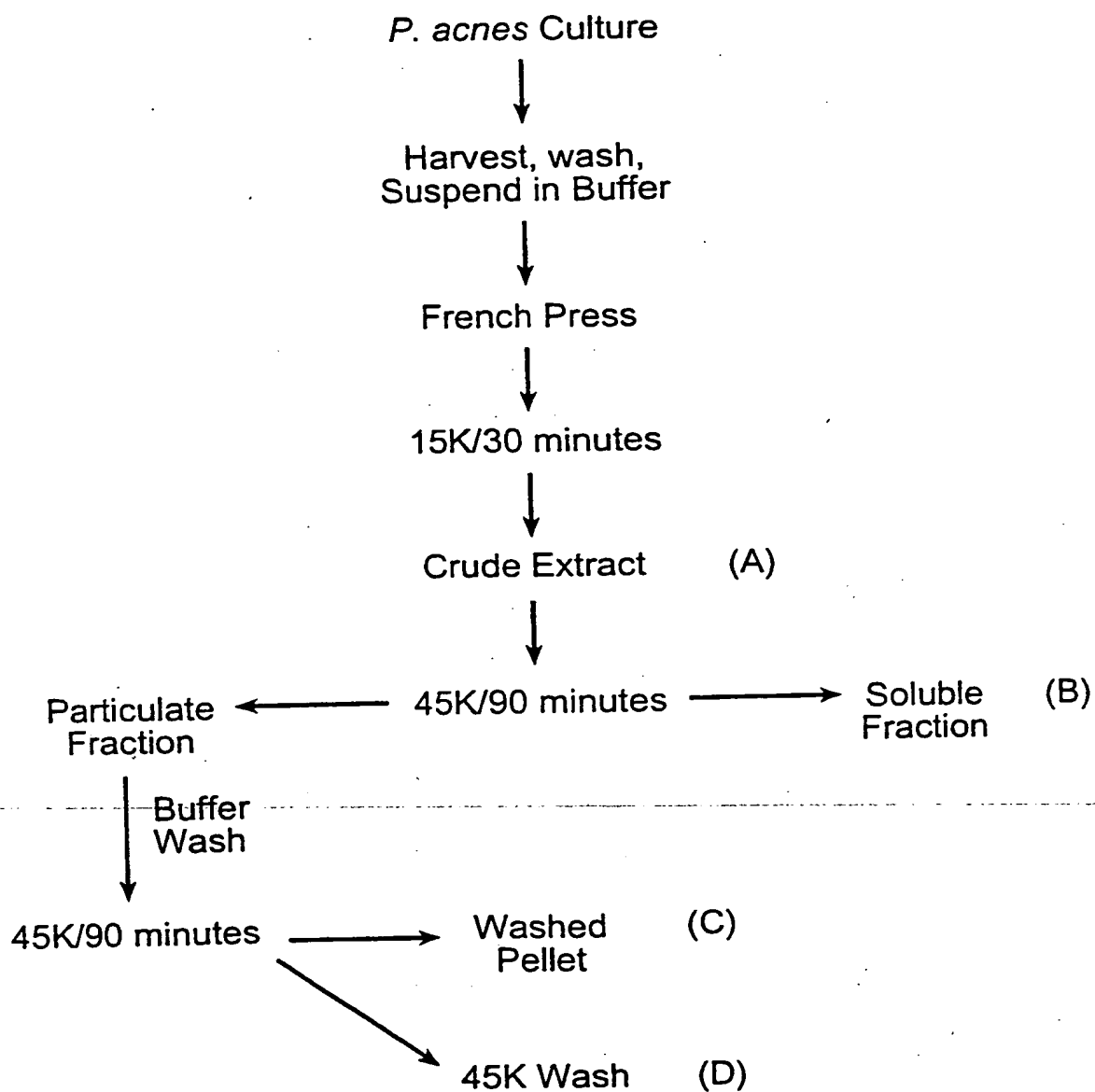


FIG.15

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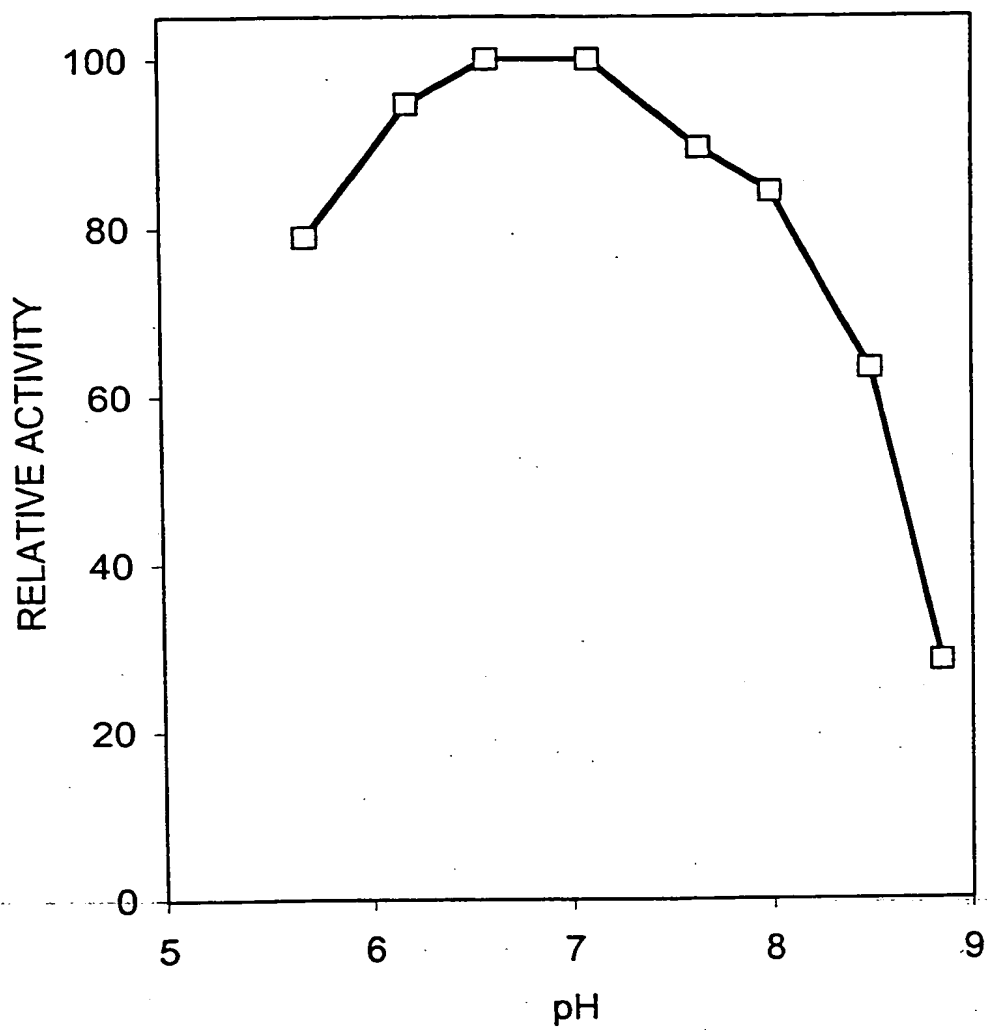


FIG. 16

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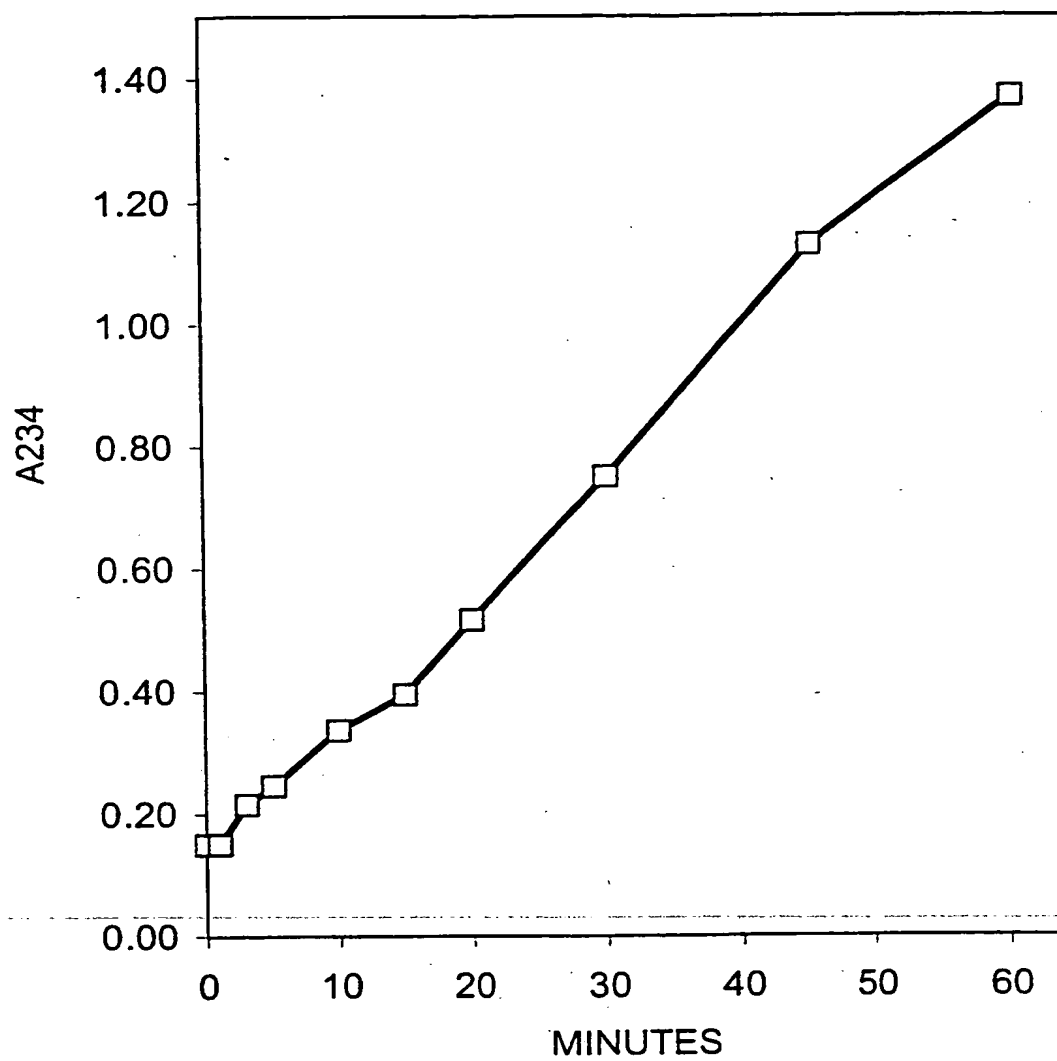


FIG. 17

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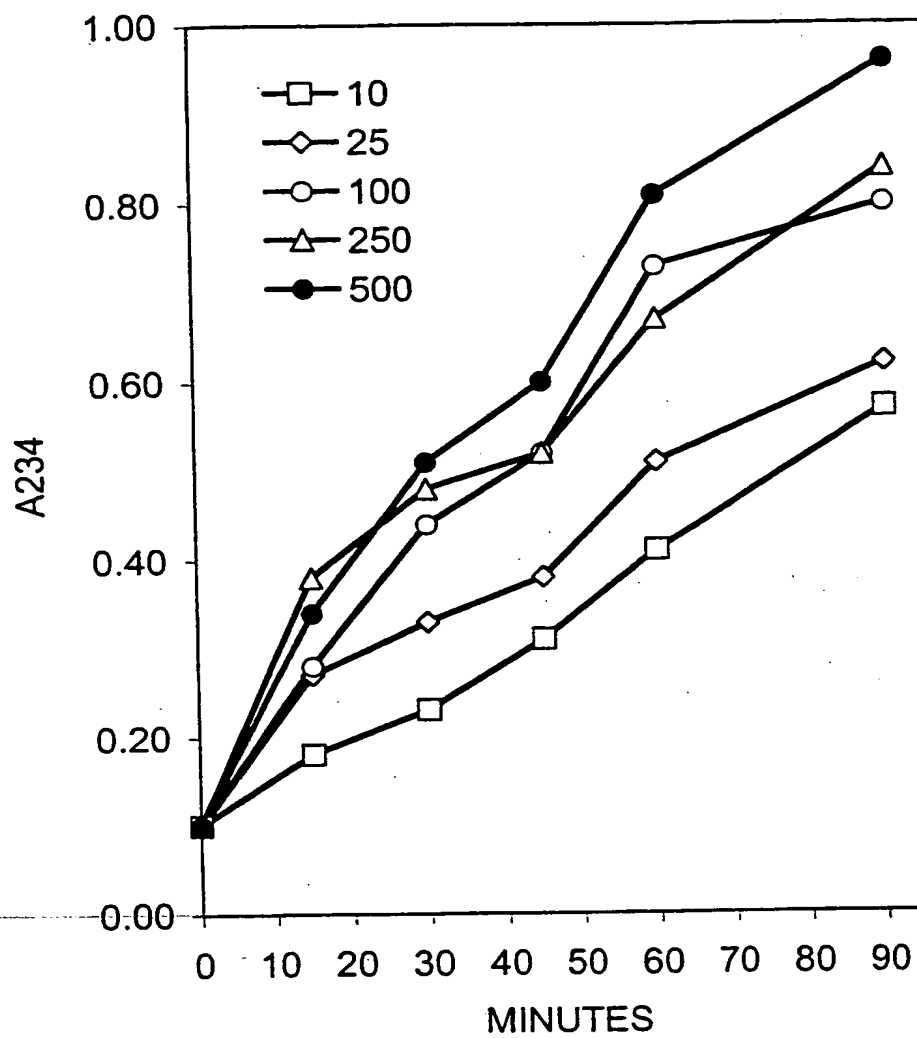


FIG. 18

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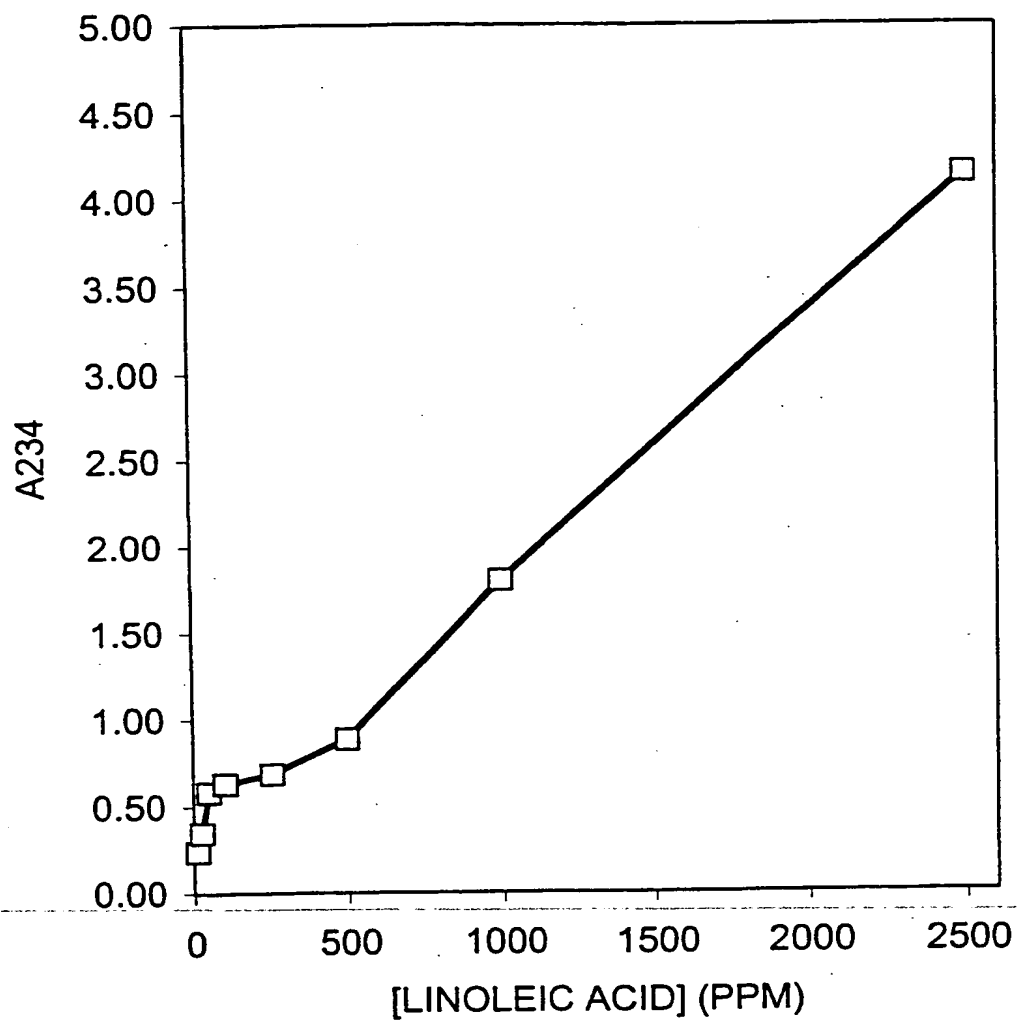


FIG. 19

20/59

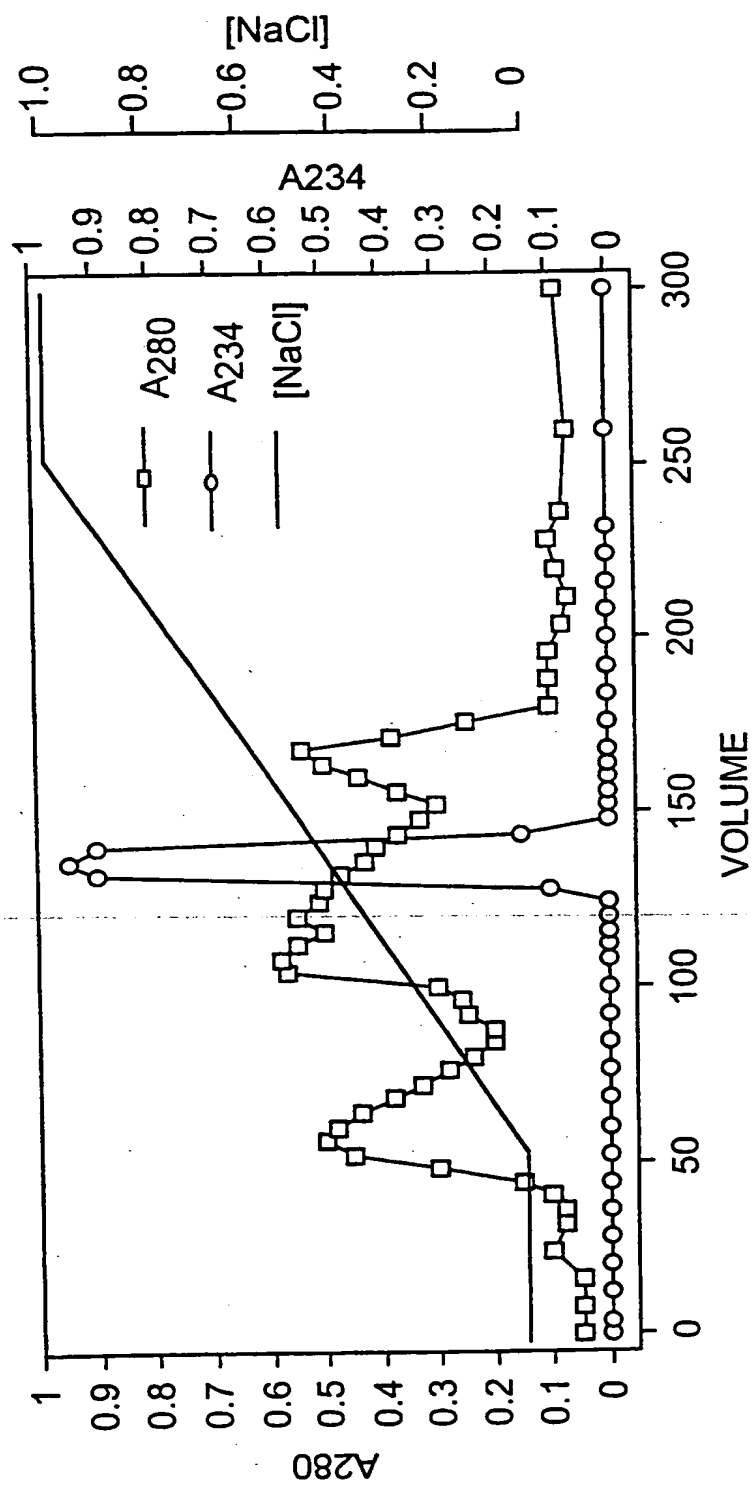


FIG. 20

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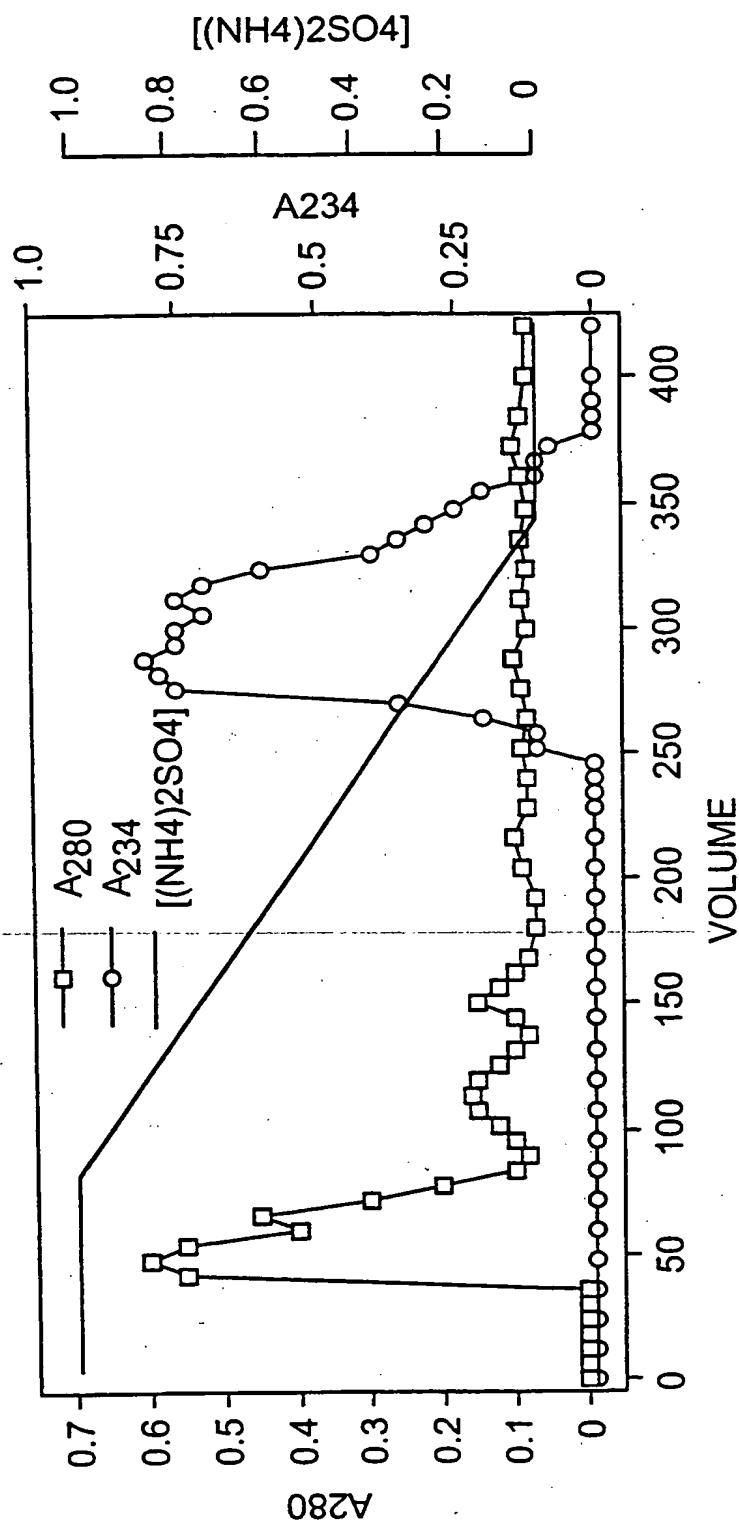


FIG. 21

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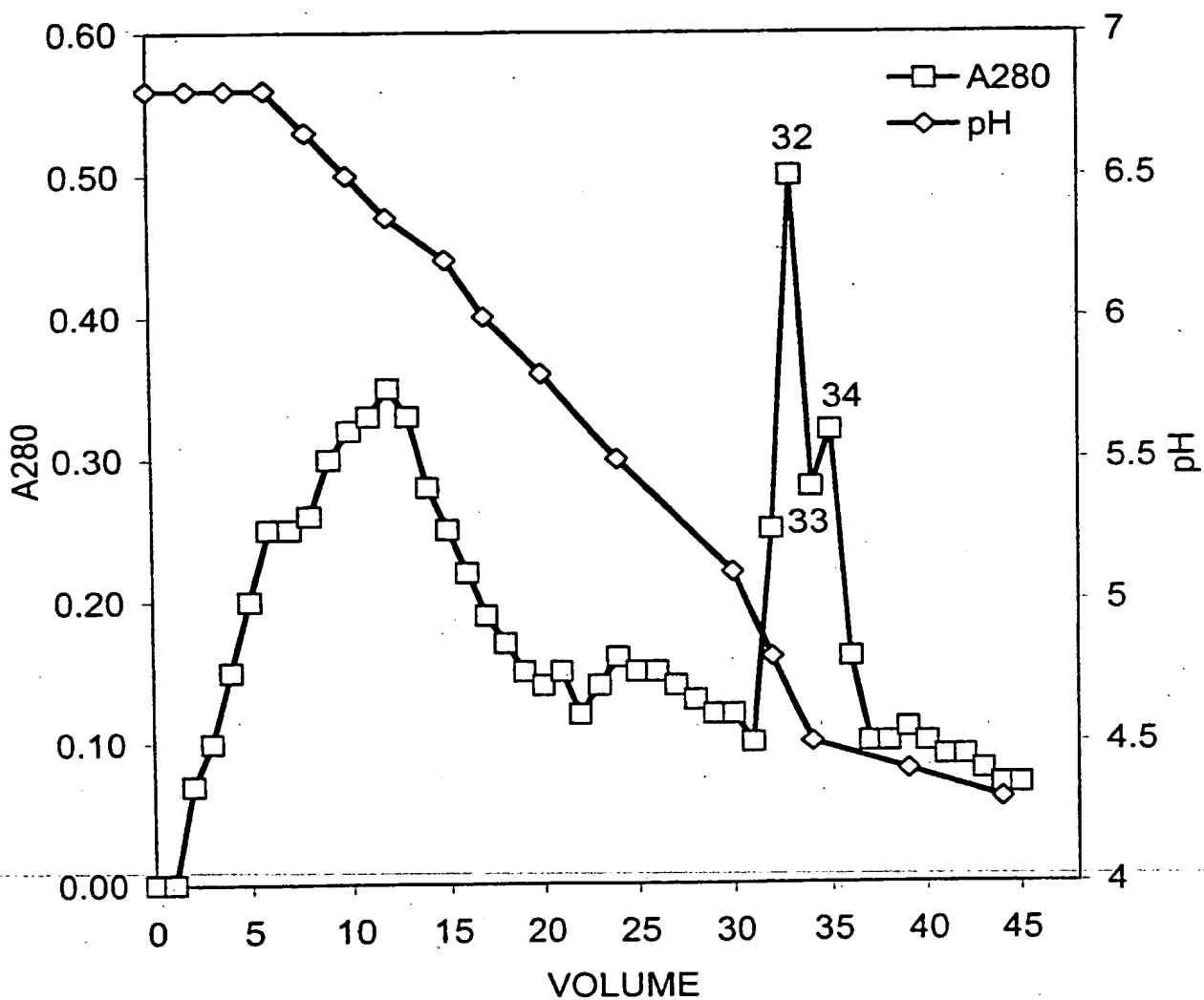


FIG. 22

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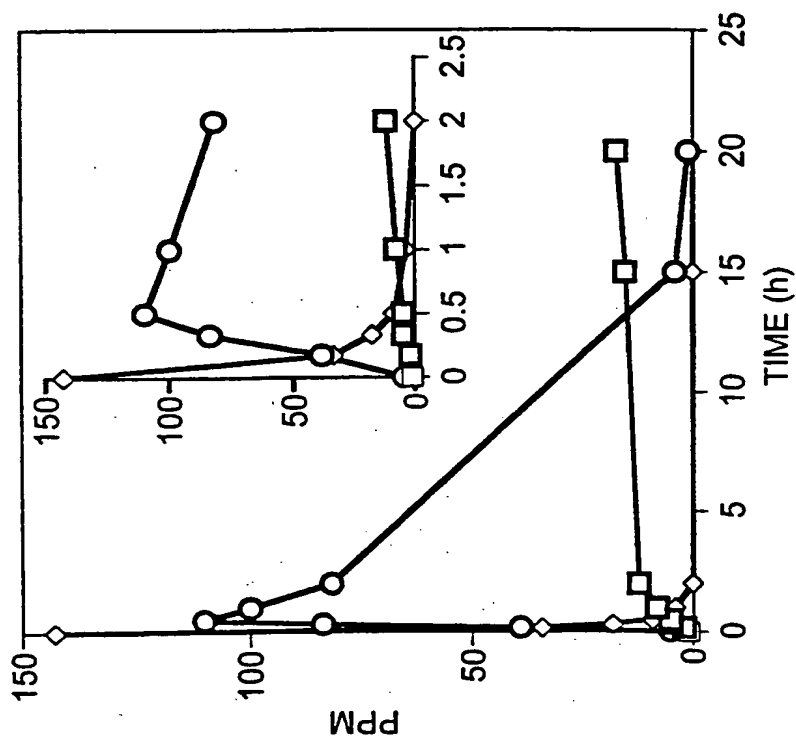


FIG. 23B

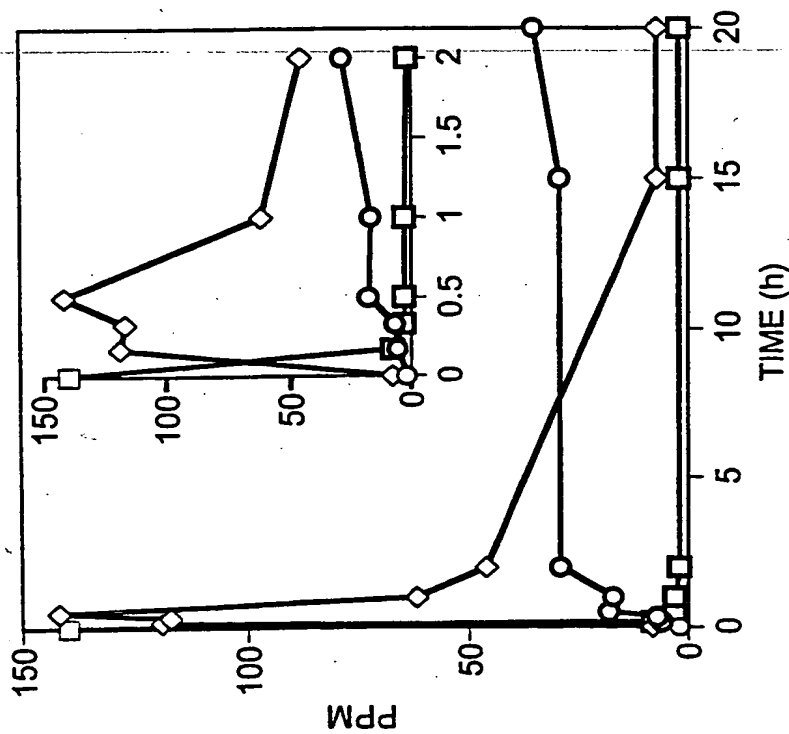


FIG. 23A

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Data whole/37°C /Aerobic

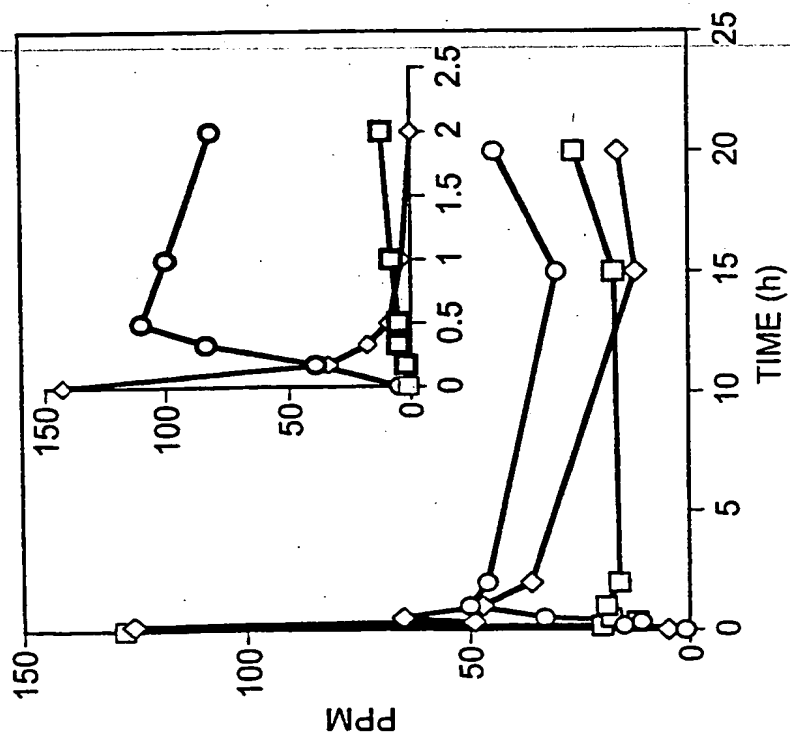


FIG. 23C

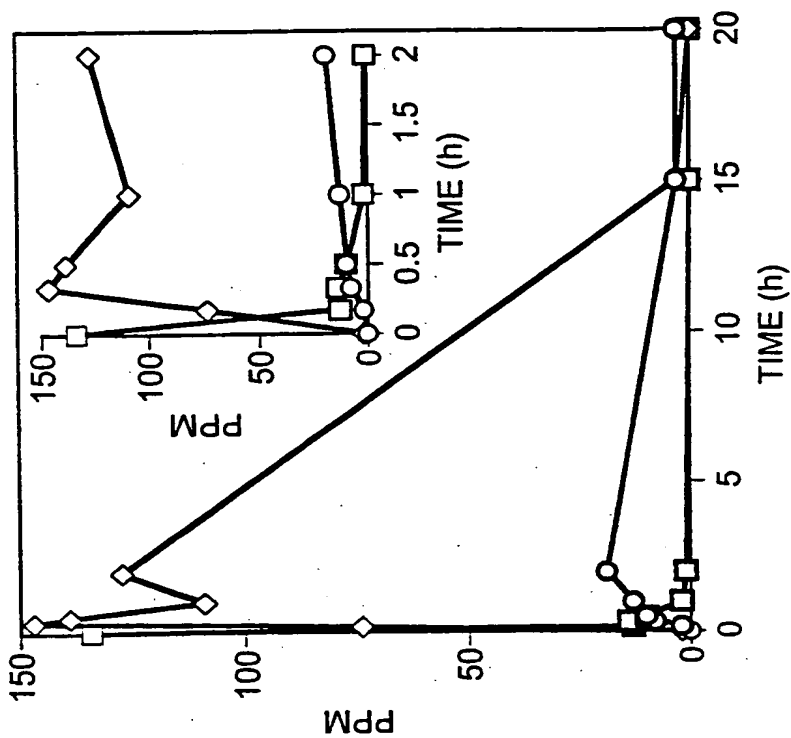


FIG. 23D

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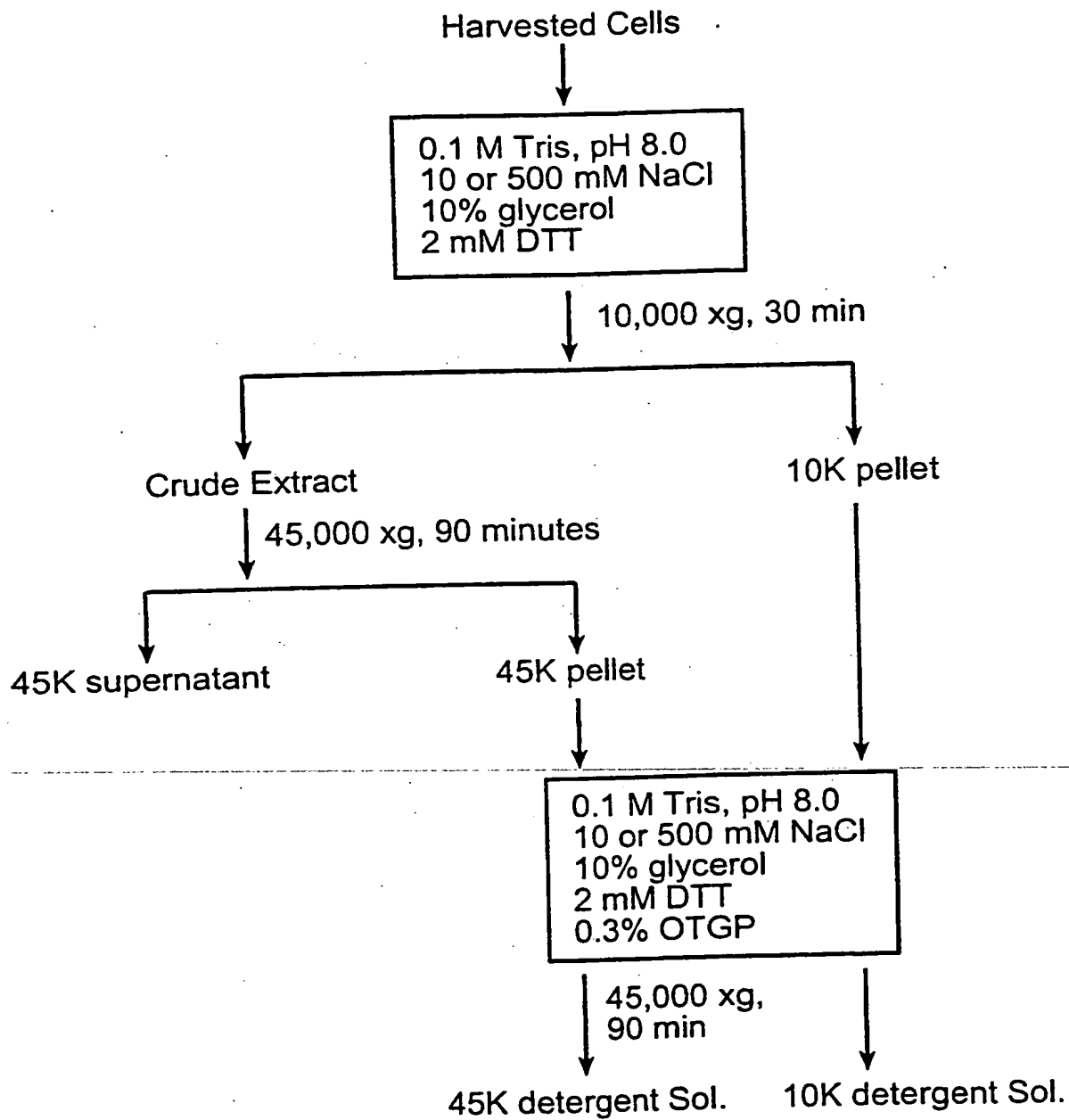


FIG. 24

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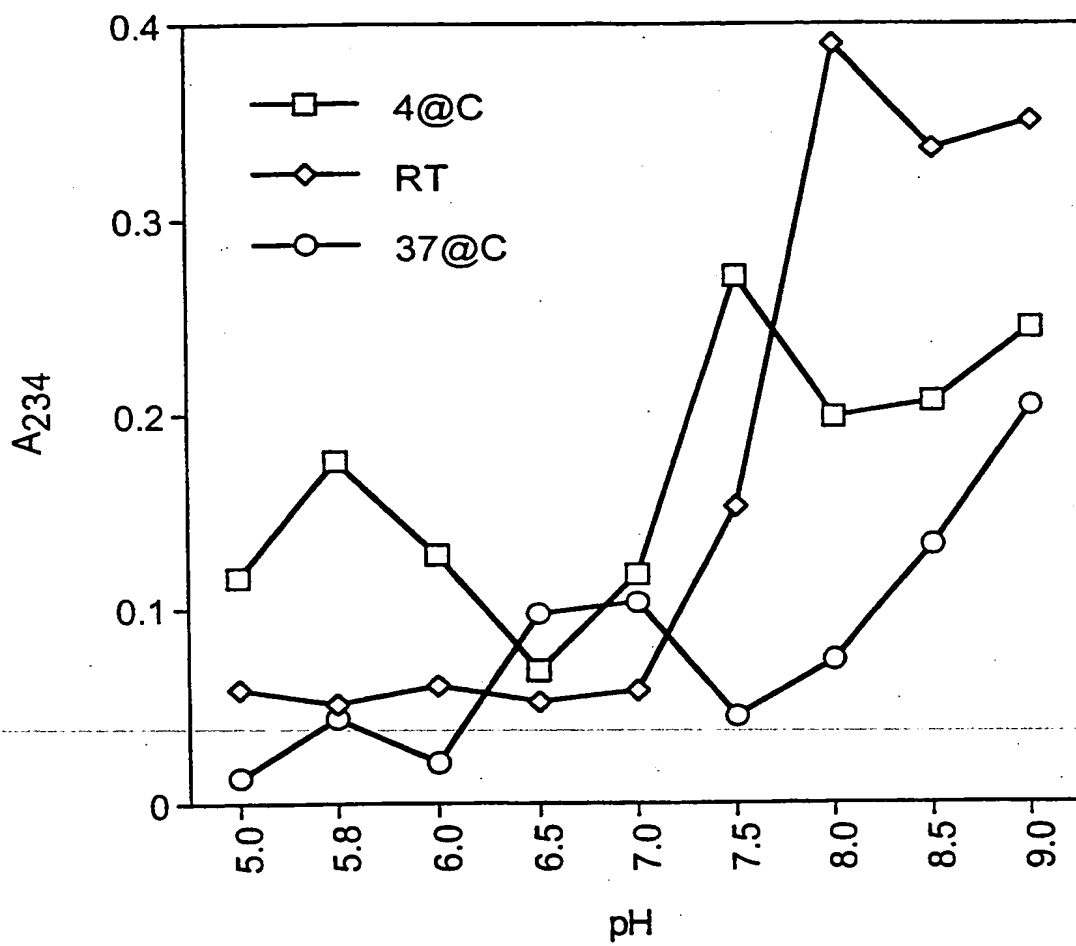


FIG. 25

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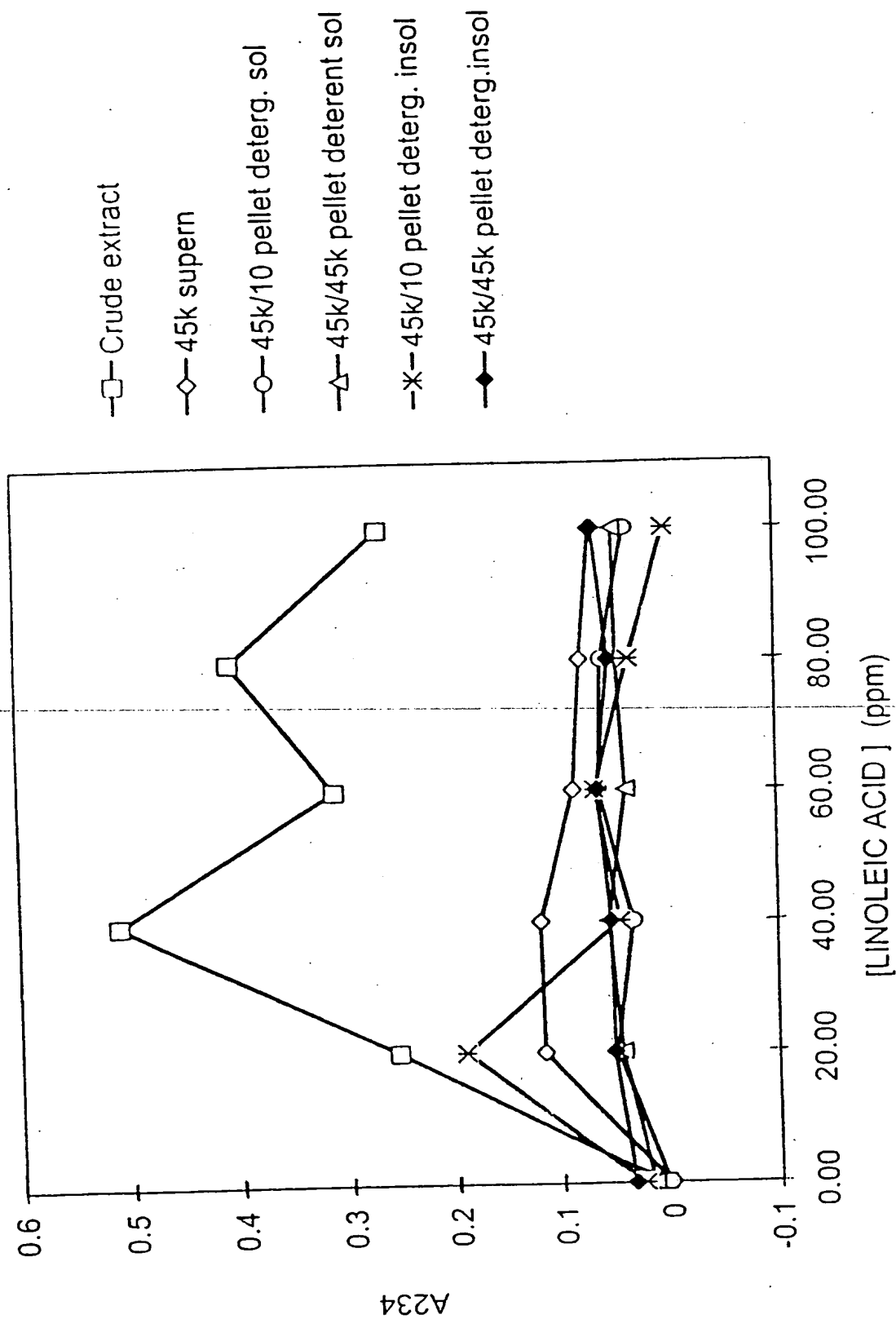


FIG. 26

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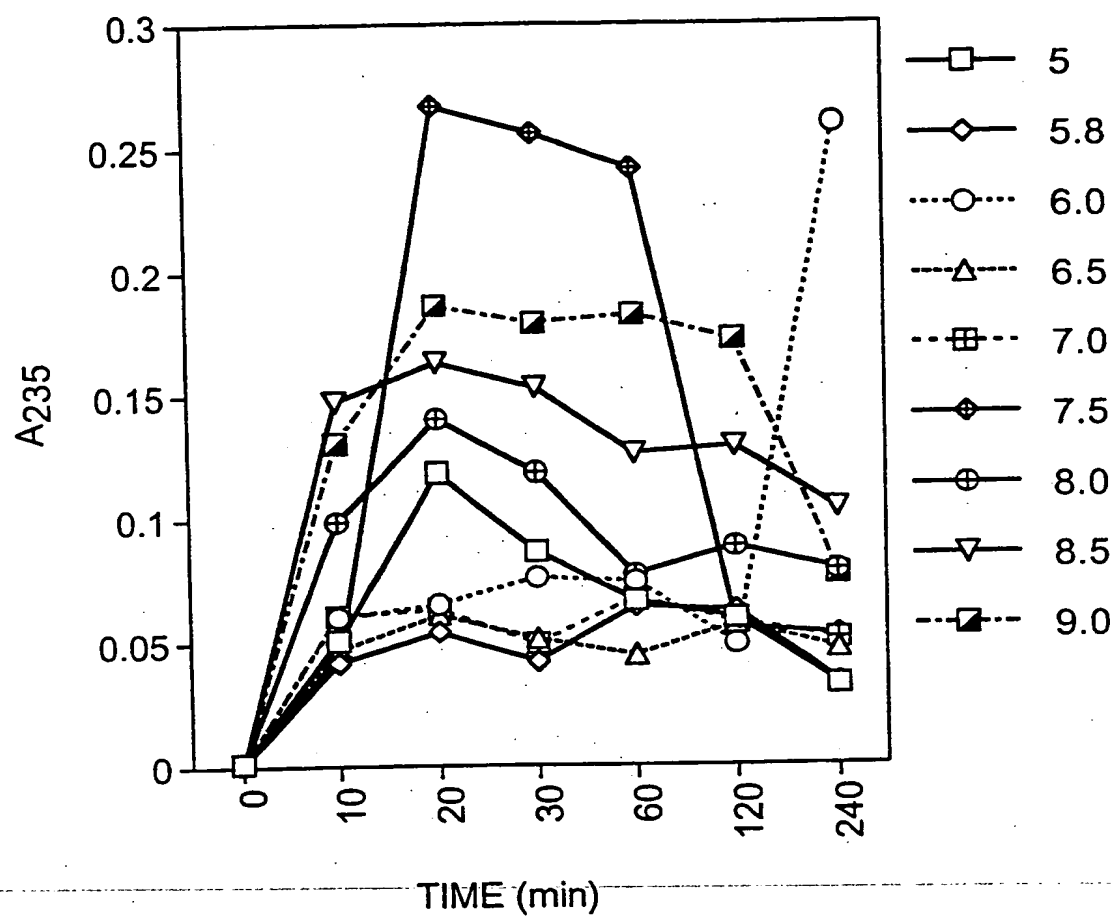


FIG. 27

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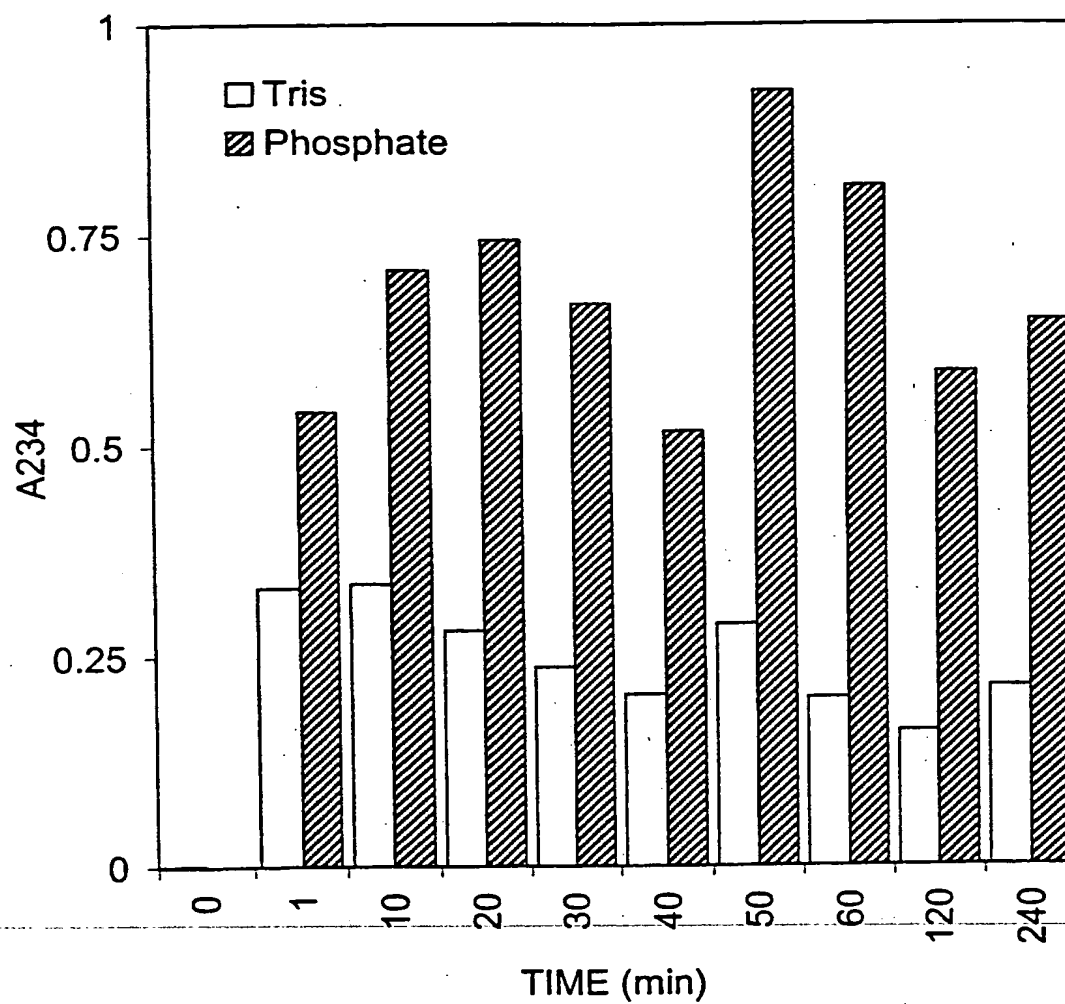


FIG. 28

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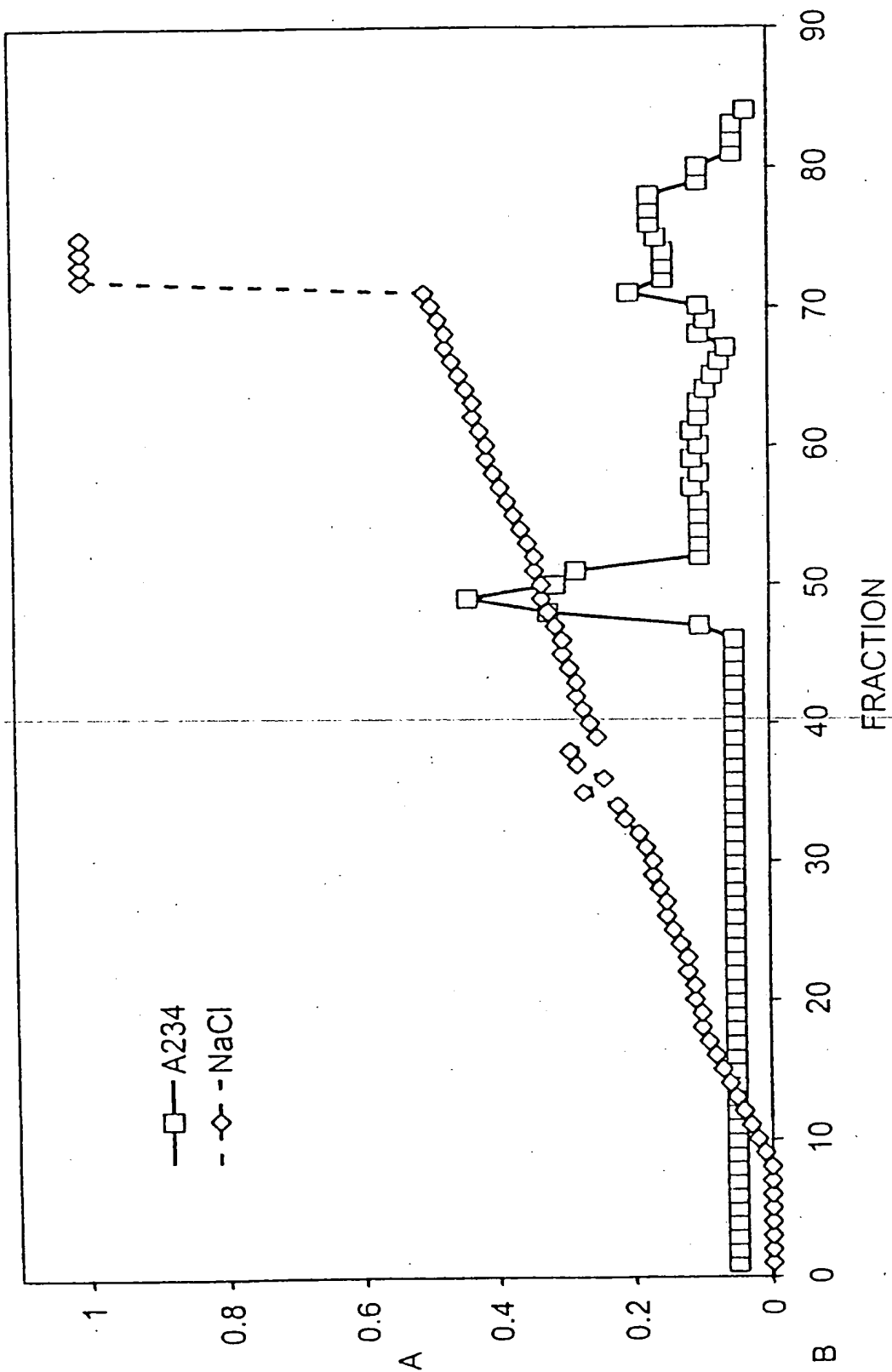


FIG. 29

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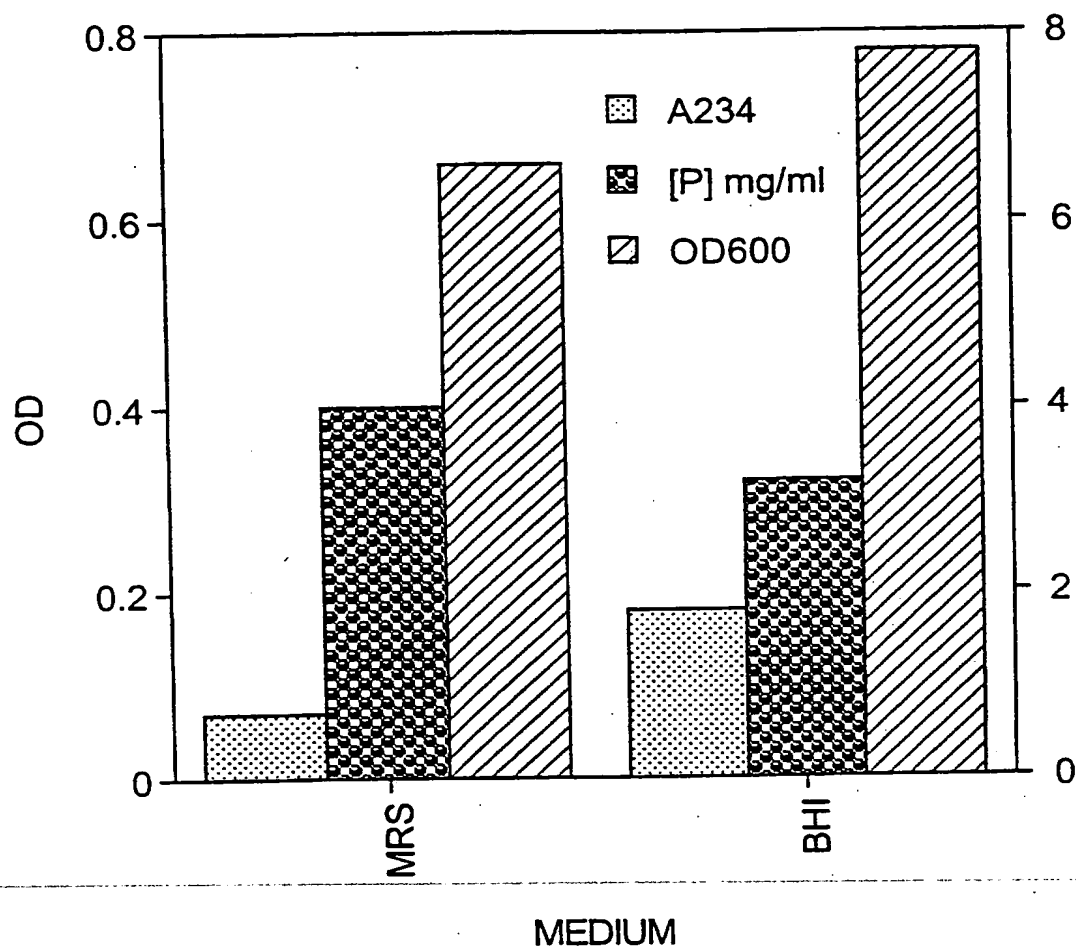


FIG. 30

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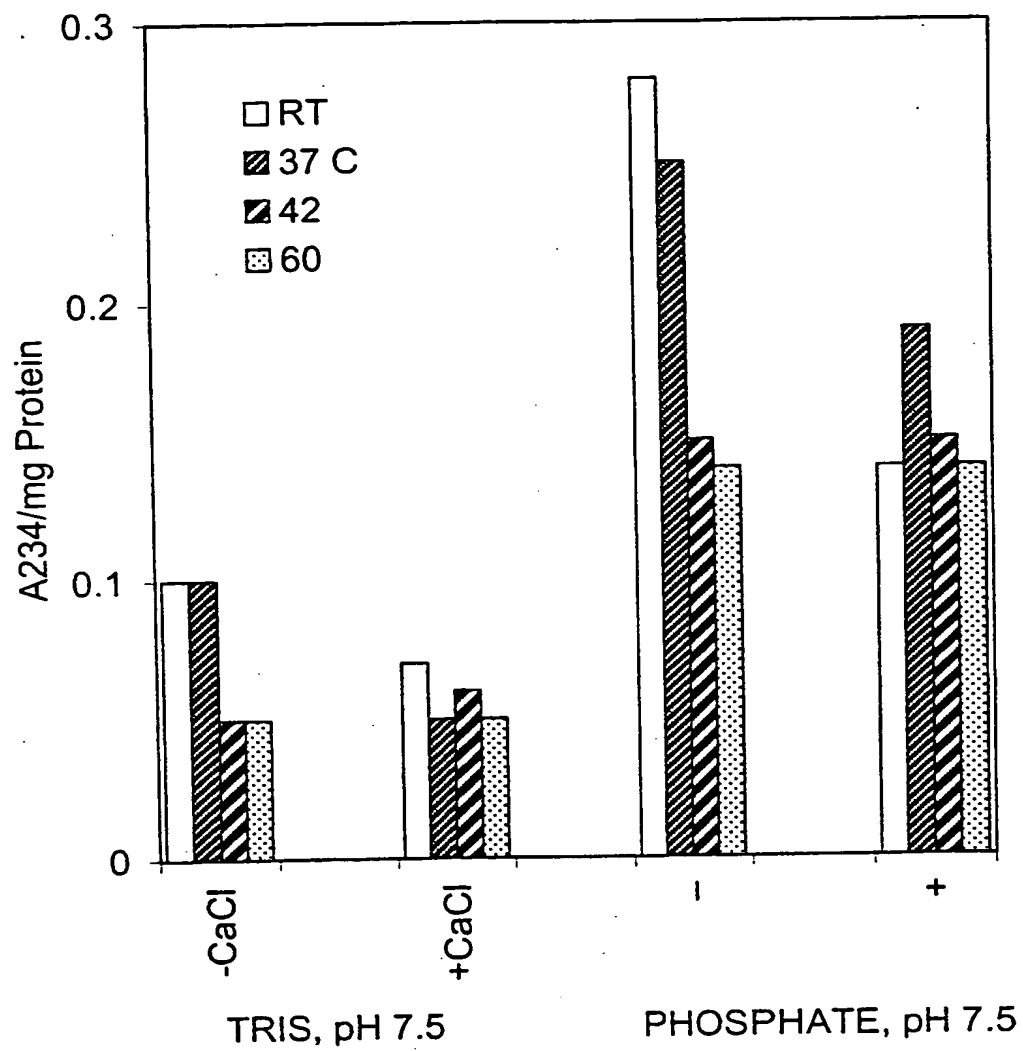


FIG. 31

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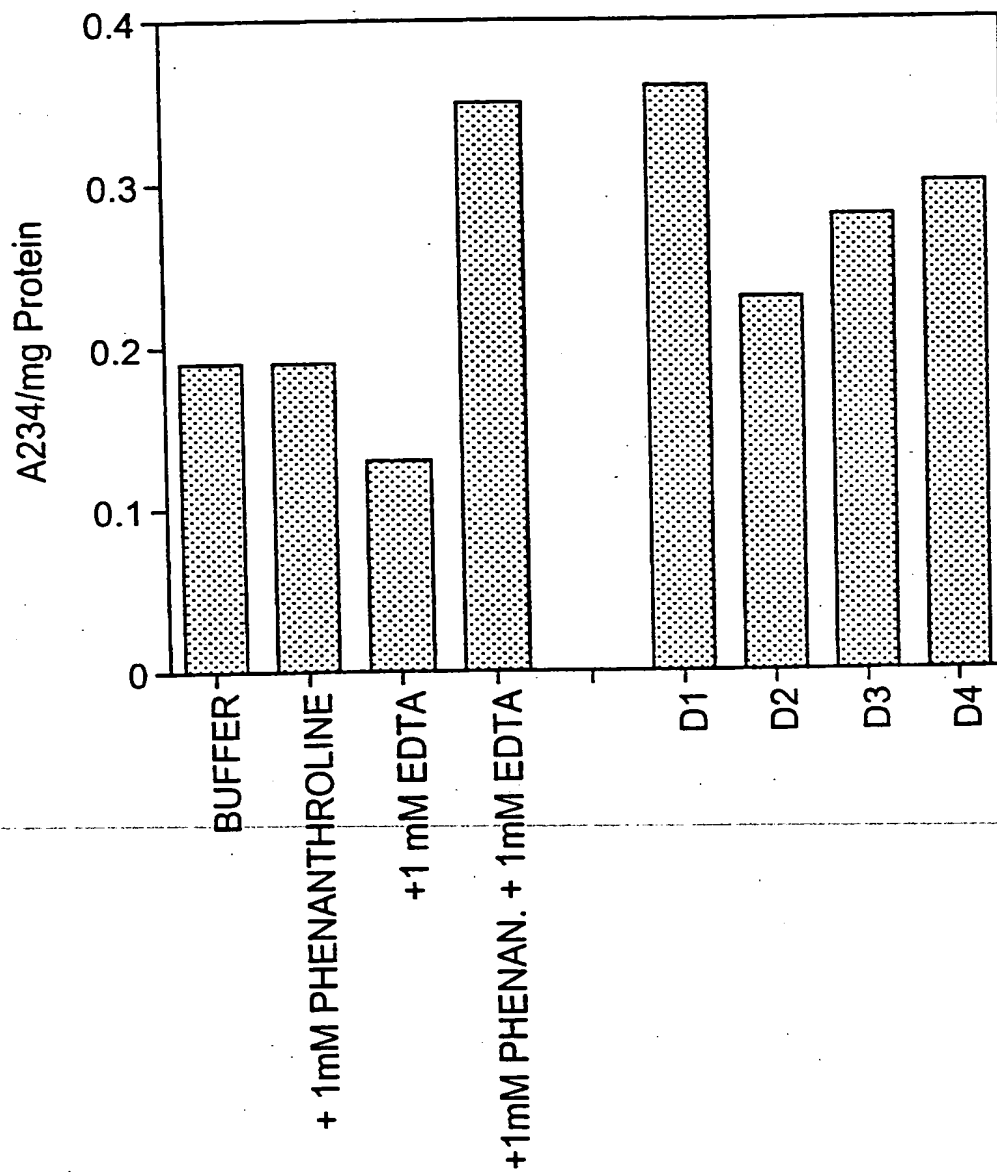


FIG. 32

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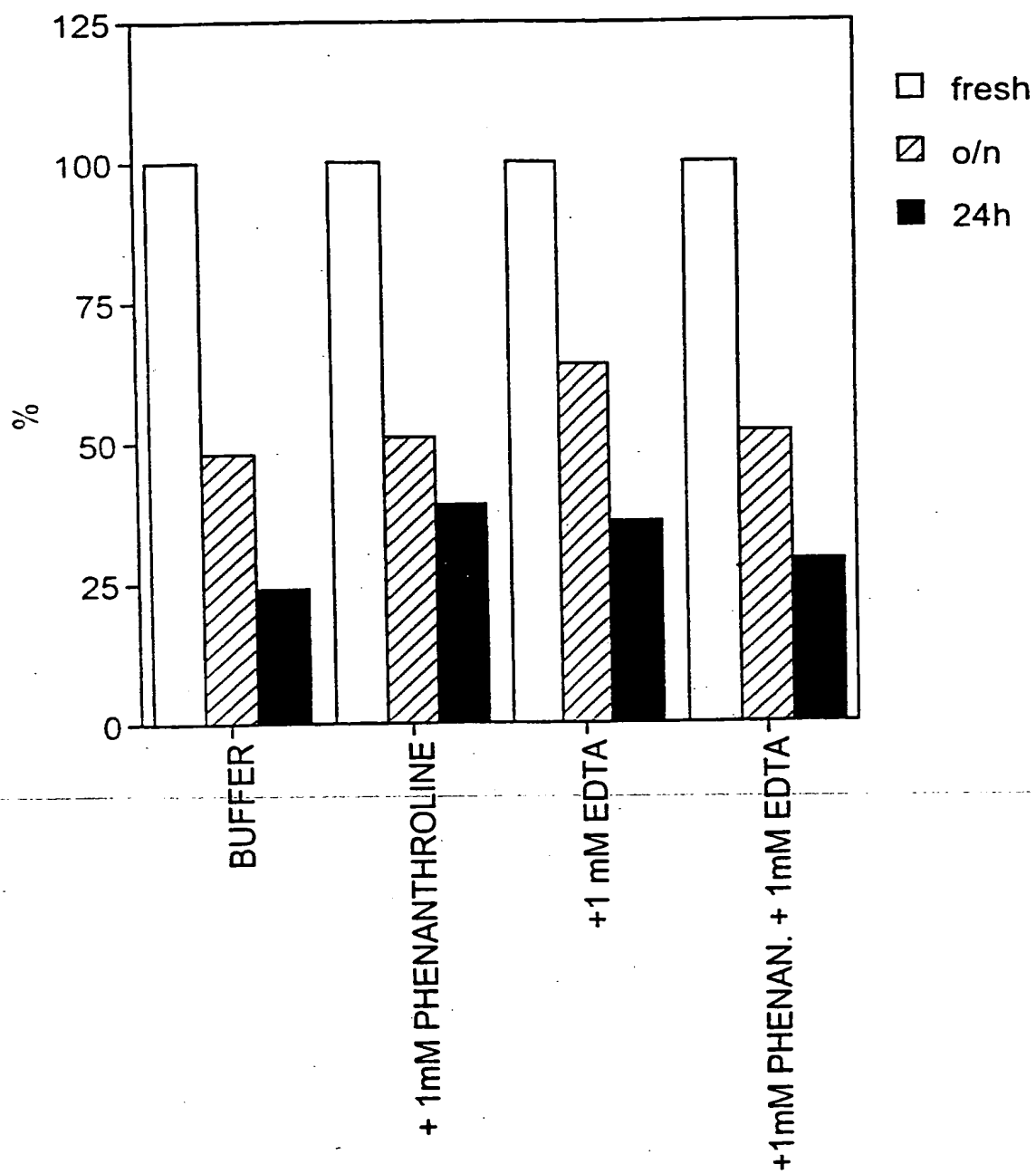


FIG. 33

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pH Effect on Extraction Efficiency of Isomerase

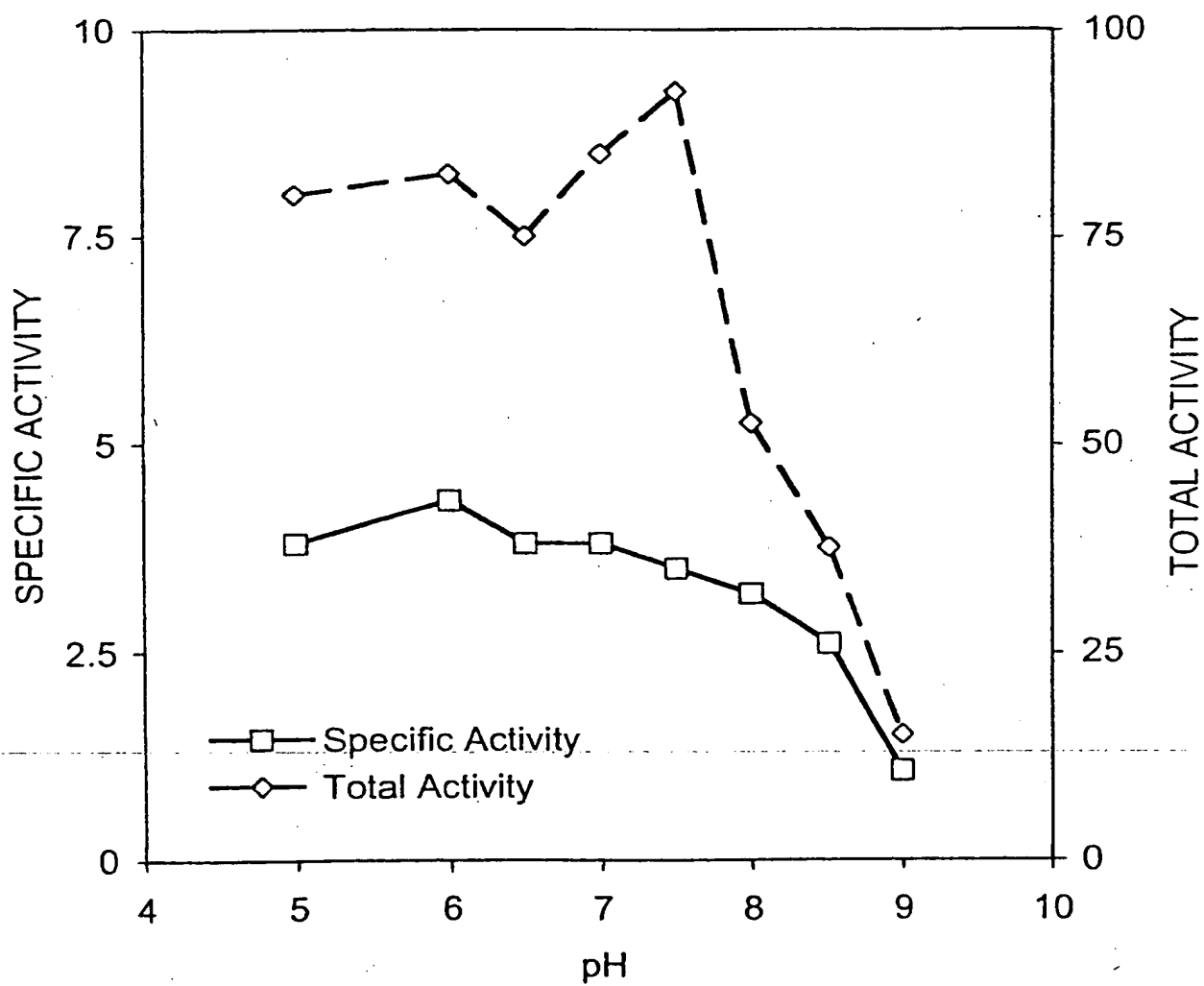


FIG. 34

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Half Lives of Isomerase vs pH

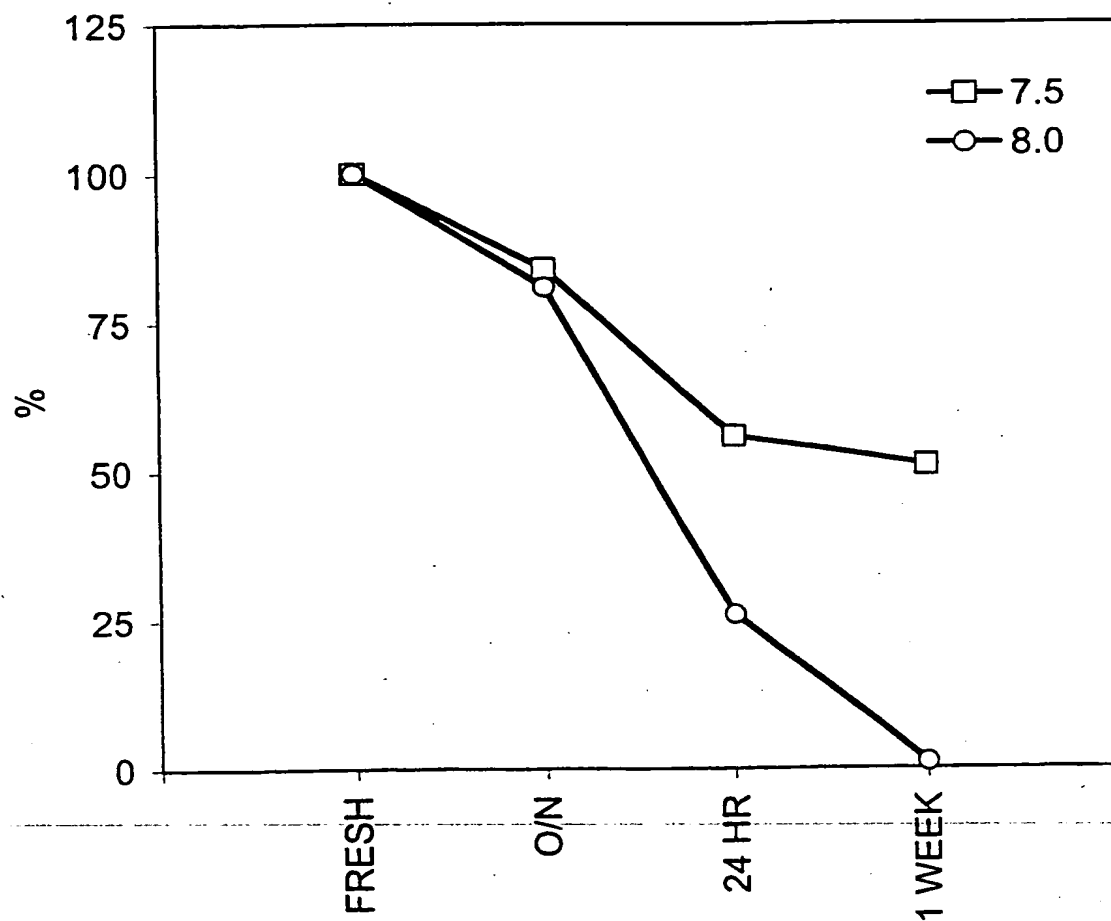


FIG. 35

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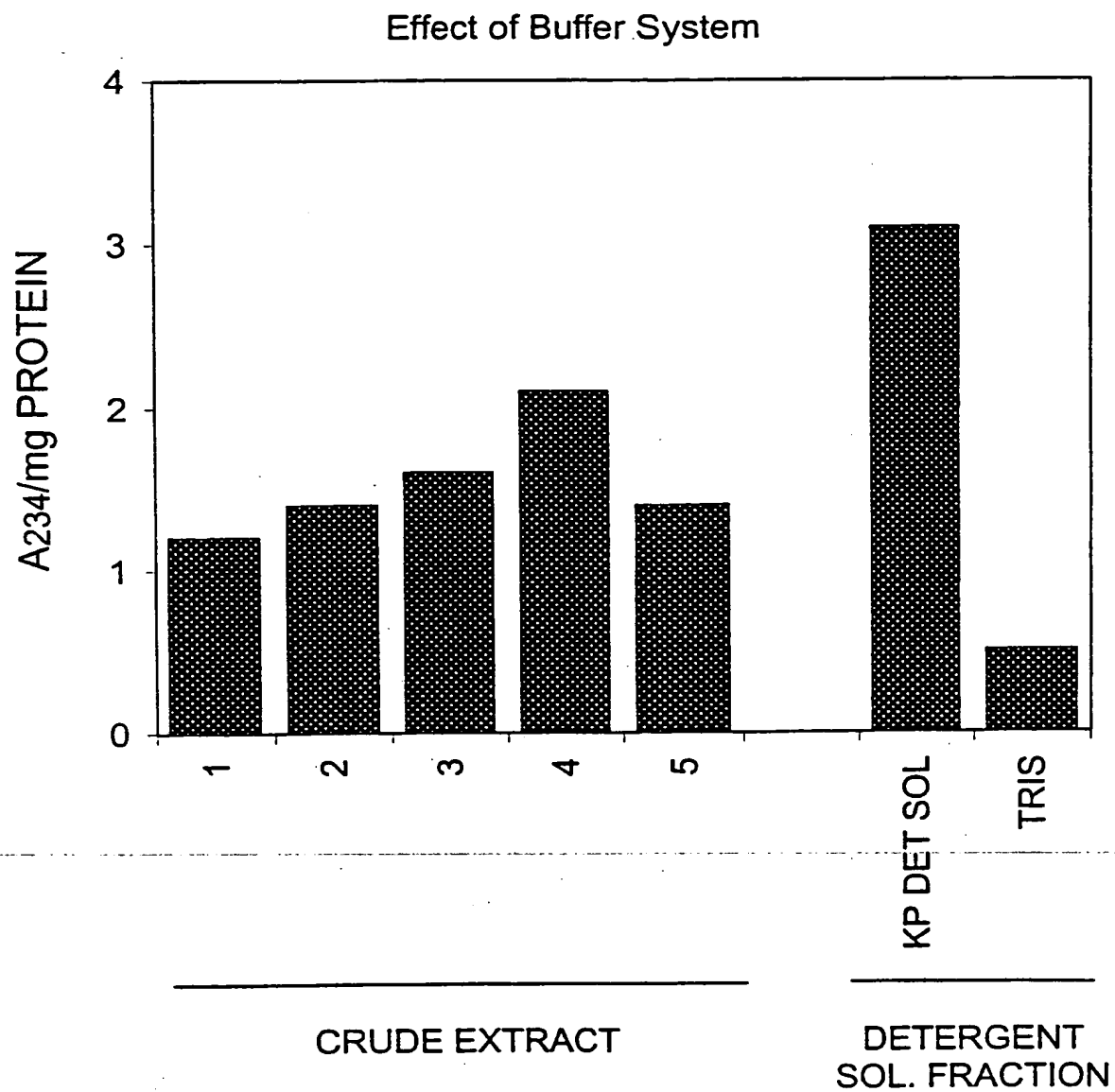


FIG. 36

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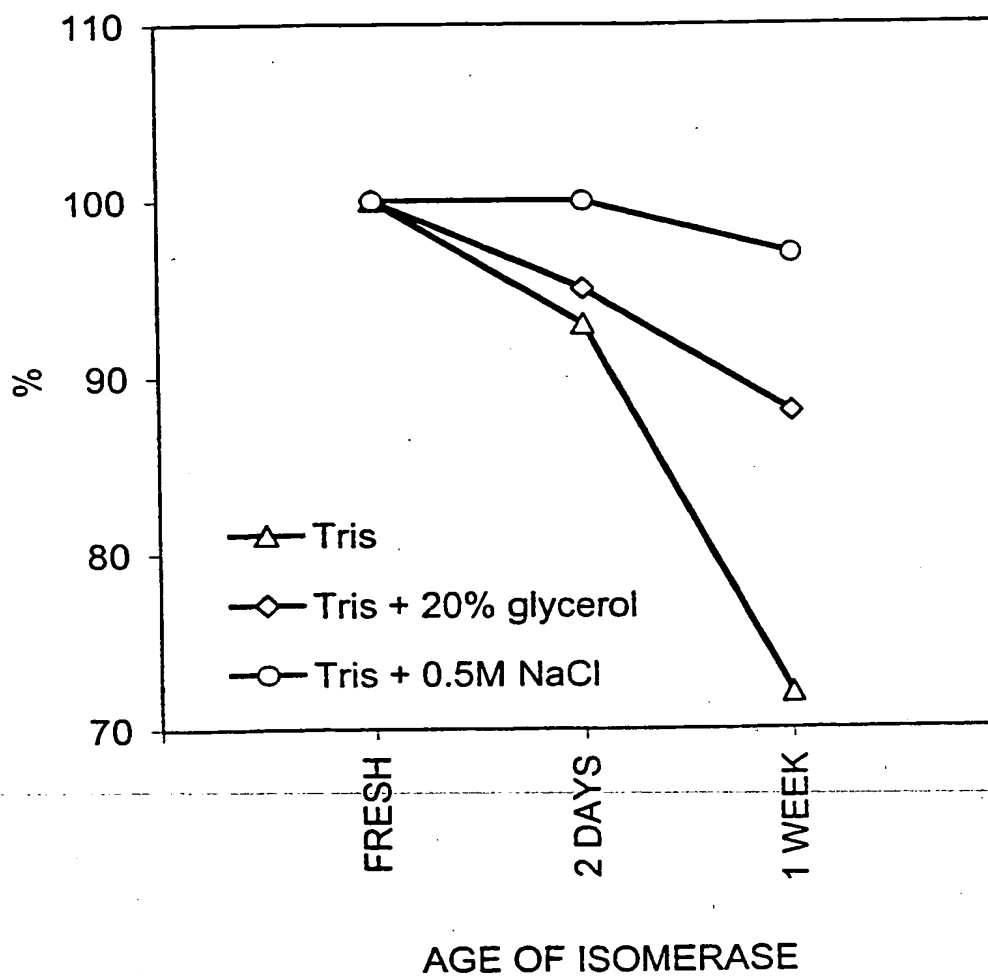
Effect of Glycerol and Salt Concentration
on Isomerase Stability

FIG. 37

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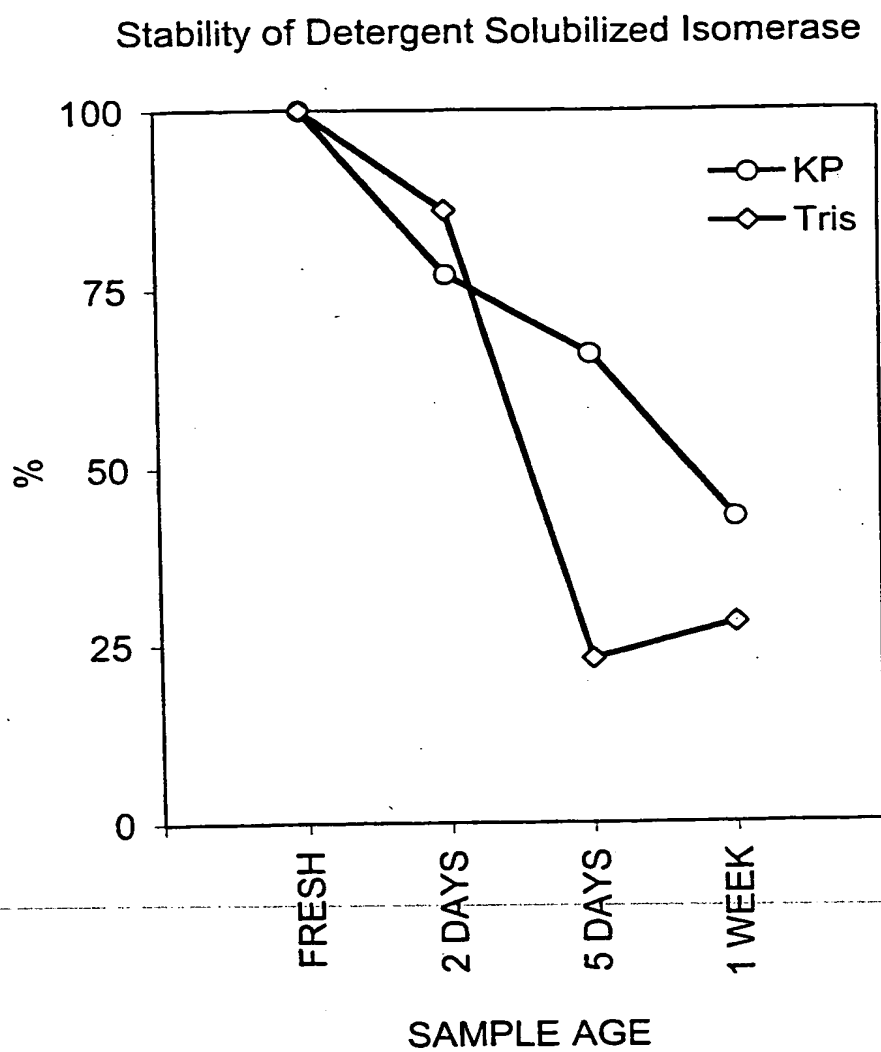


FIG. 38

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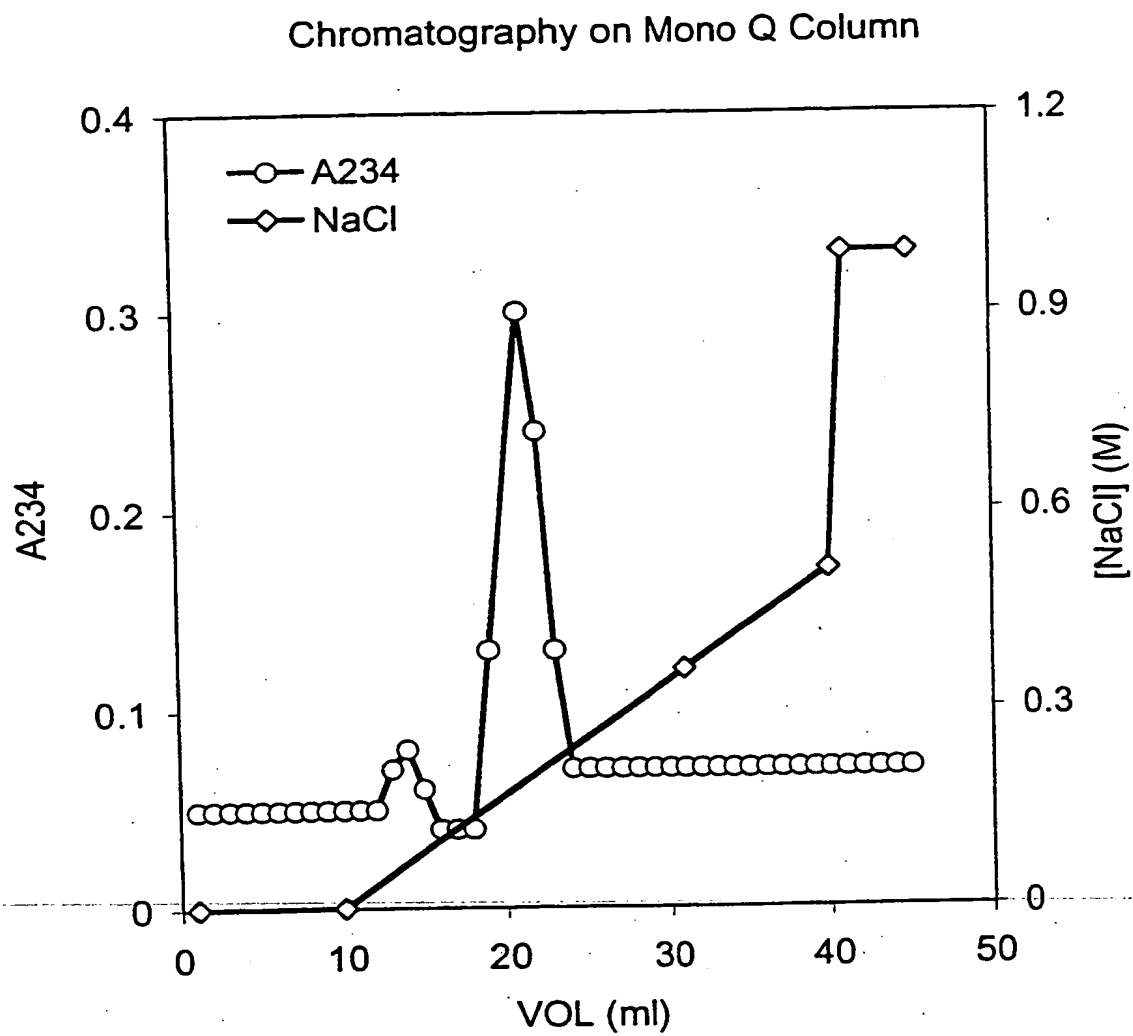


FIG. 39

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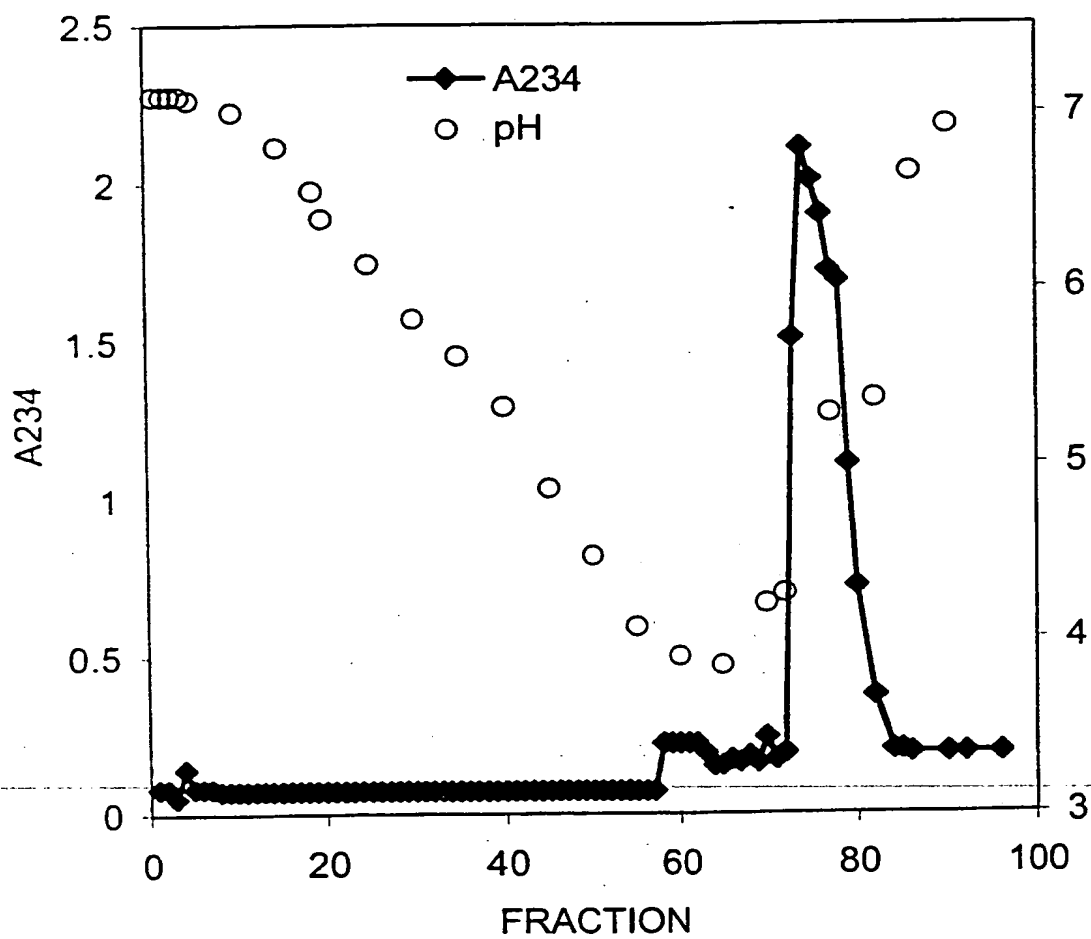
Separation of Partially Purified Isomerase
by Chromatofocusing

FIG. 40

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Chromatography of Detergent Solubilized Isomerase
on DEAE-5PW Column

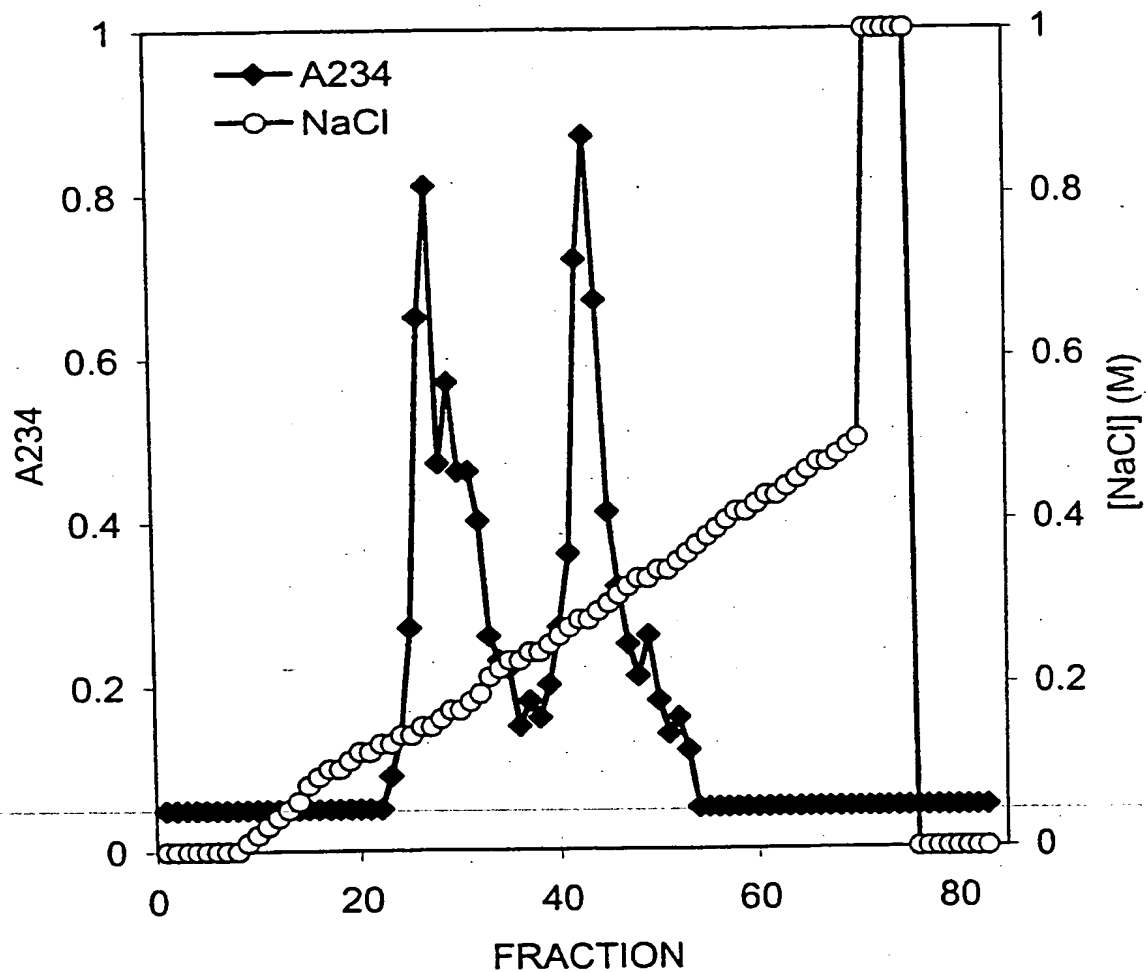
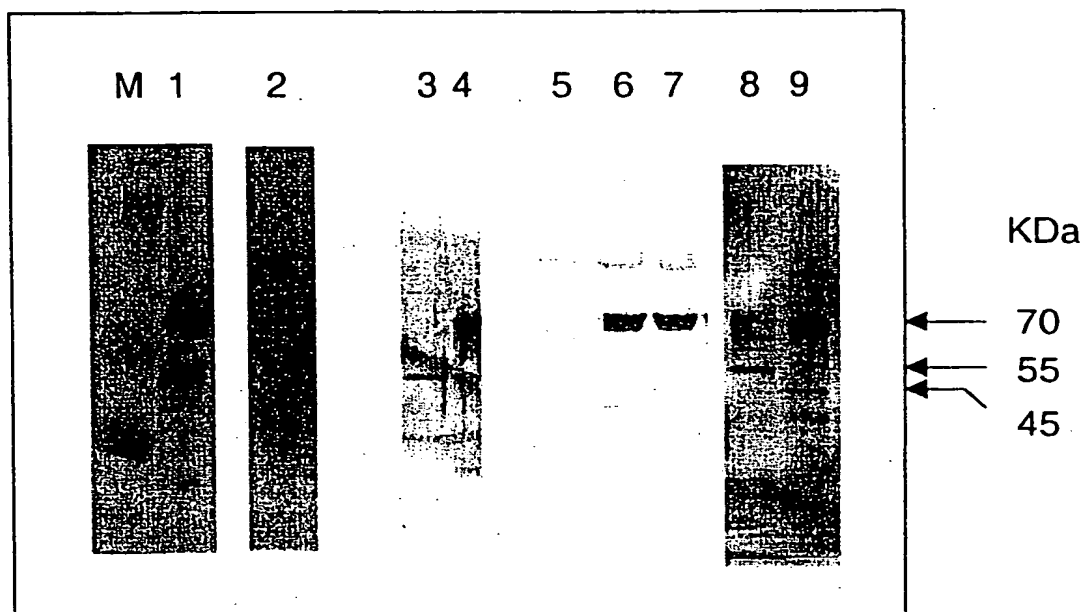


FIG. 41

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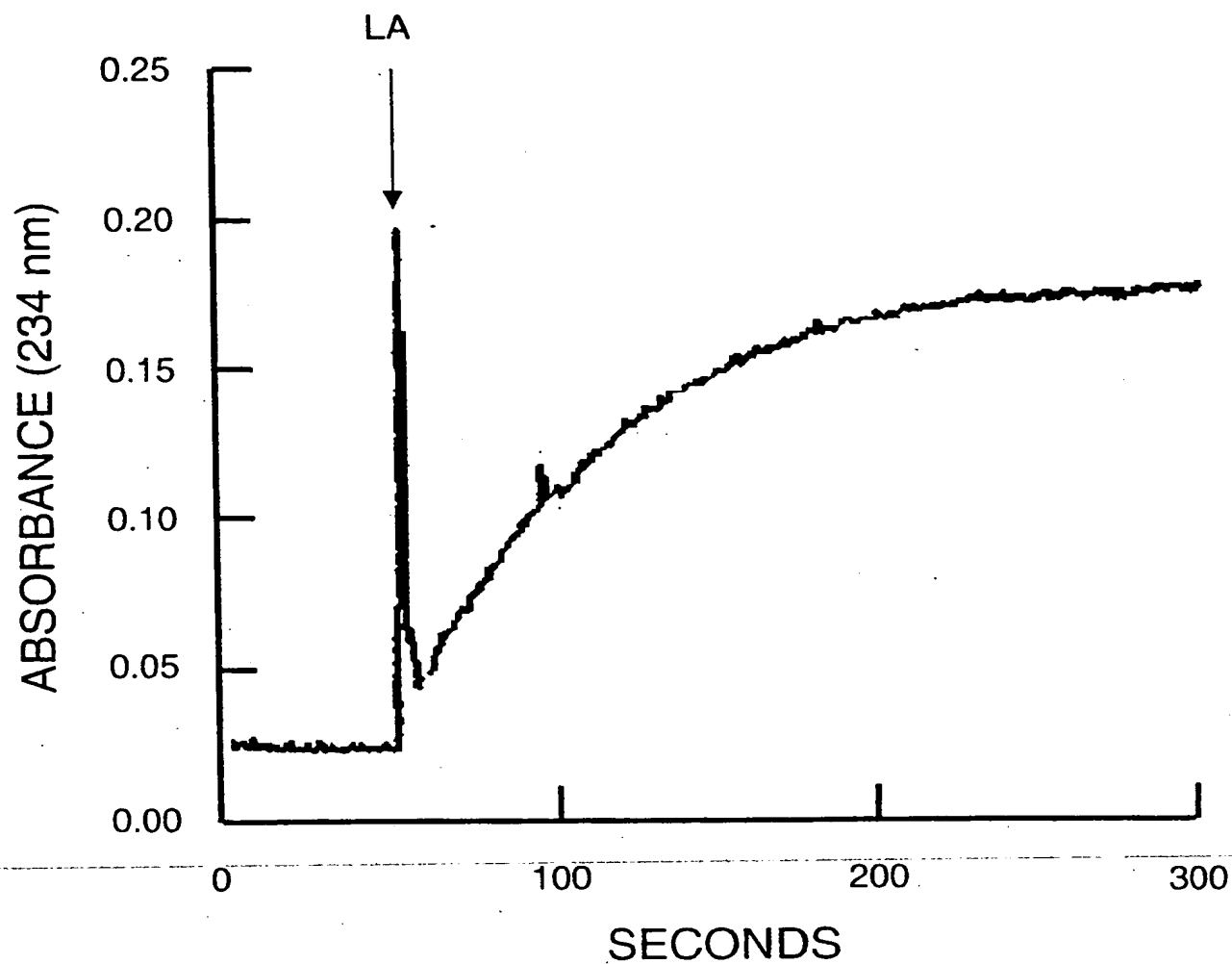
Western Blot analysis of linoleate isomerase using rabbit antibodies specific for the cloned *L. reuteri* PYR8 isomerase. Total protein of cell lysates prepared from different strains was used in the analysis.

M. Protein size marker

1. *E. coli* expressing the isomerase-histag fusion protein
2. *L. reuteri* PYR8
3. *B. subtilis* wild type
4. *B. subtilis* transformed with the vector pBH1 containing the isomerase gene under HpaII promoter control
5. *L. reuteri* 23272 wild type
6. *L. reuteri* 23272 transformed with the vector pTRKH2 containing the isomerase gene under the control of both its native promoter and the *lac* promoter
7. *L. reuteri* 23272 transformed with the vector pTRKH2 containing the isomerase gene under the control of its native promoter
8. *P. acnes* 6919
9. *C. sporogenes* 23272

FIG. 42

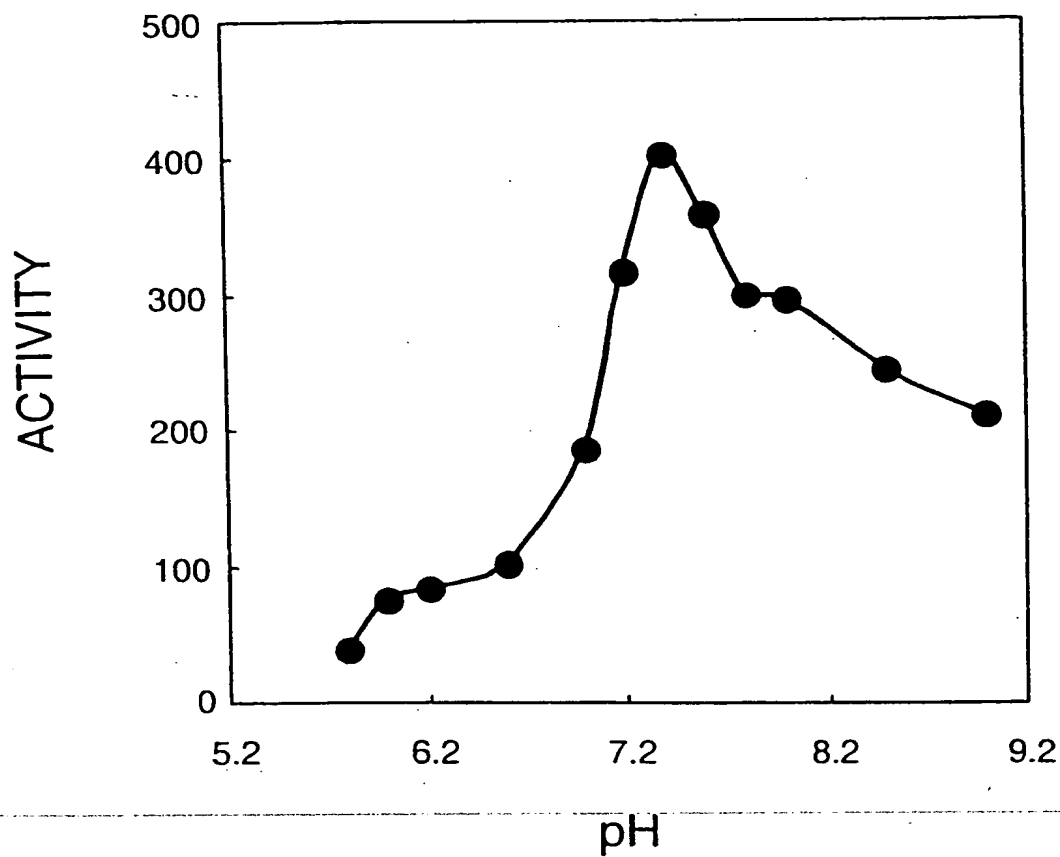
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Time course of isomerization of linoleic acid. The isomerization reaction was initiated by adding 20 μ M linoleic acid at 50 seconds.

FIG. 43

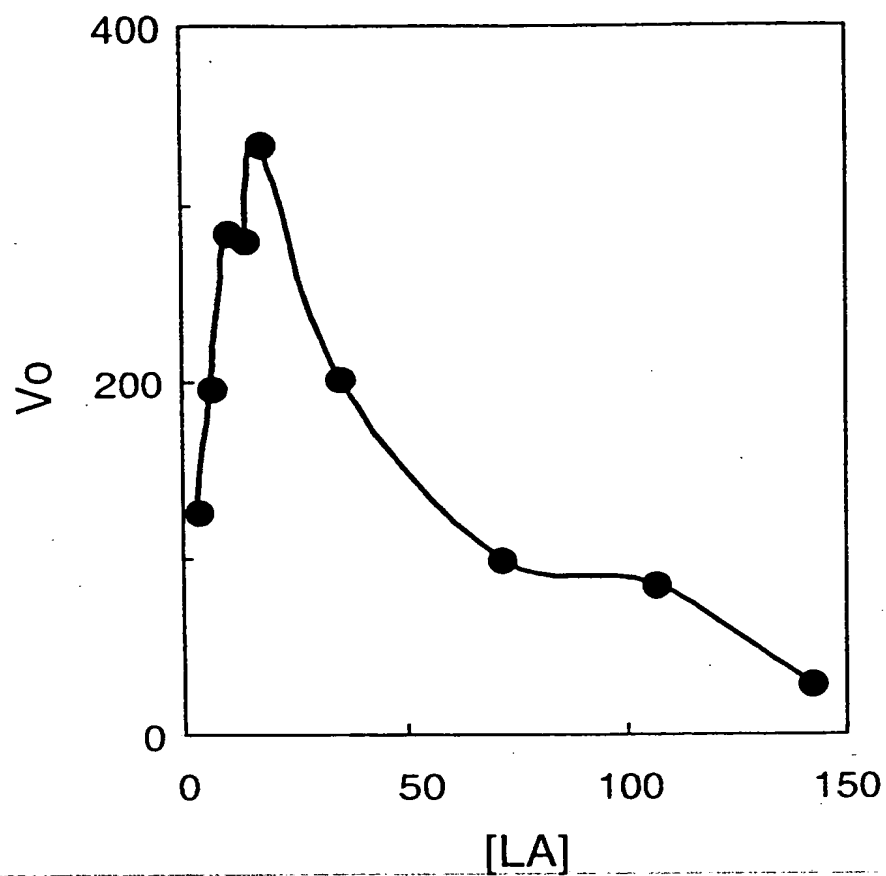
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Effect of pH on isomerization of linoleic acid to CLA by
C. sporogenes linoleate isomerase. Activity as nmol CLA/min/mg protein.

FIG. 44

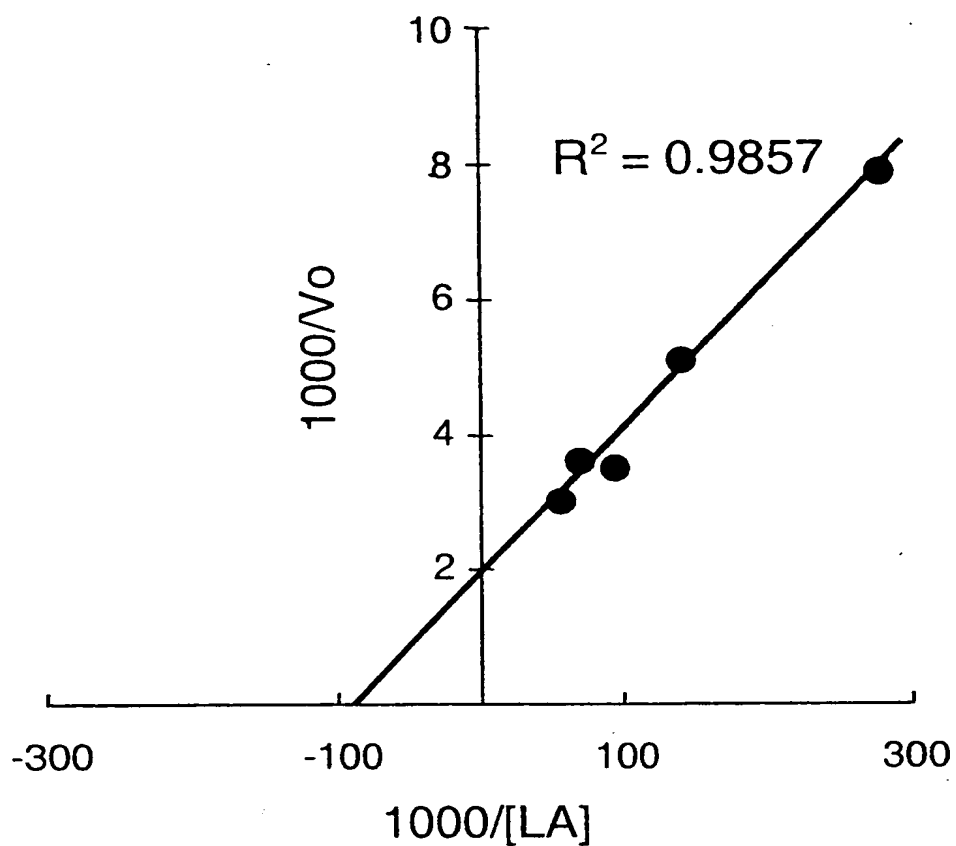
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Effect of linoleic acid concentration on the rate of isomerization.
 V_o as nmols CLA/min/mg protein. $[LA]$ as μM .

FIG. 45

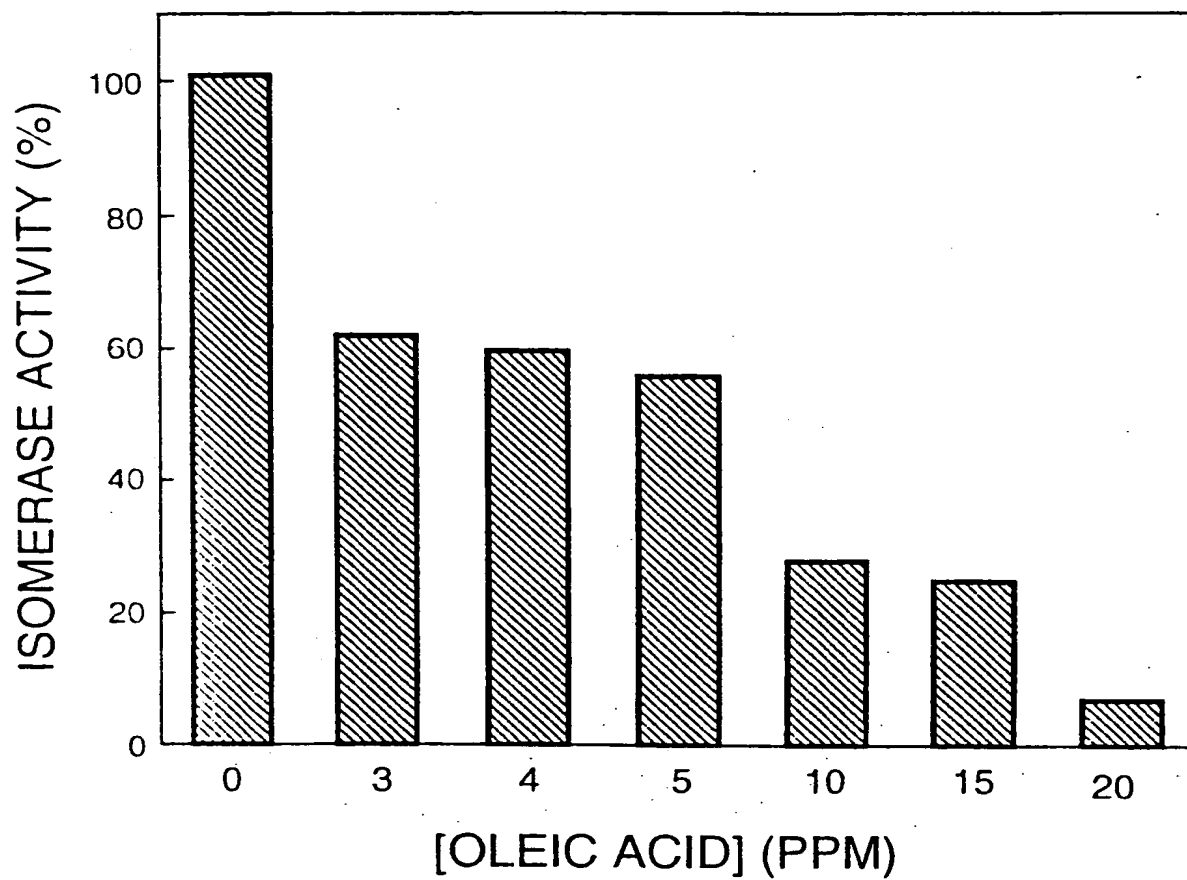
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Lineweaver-Burk plot of reaction kinetics of *C. sporogenes* linoleate isomerase. V_o as nmols CLA/min/mg protein. $[LA]$ as μM .

FIG. 46

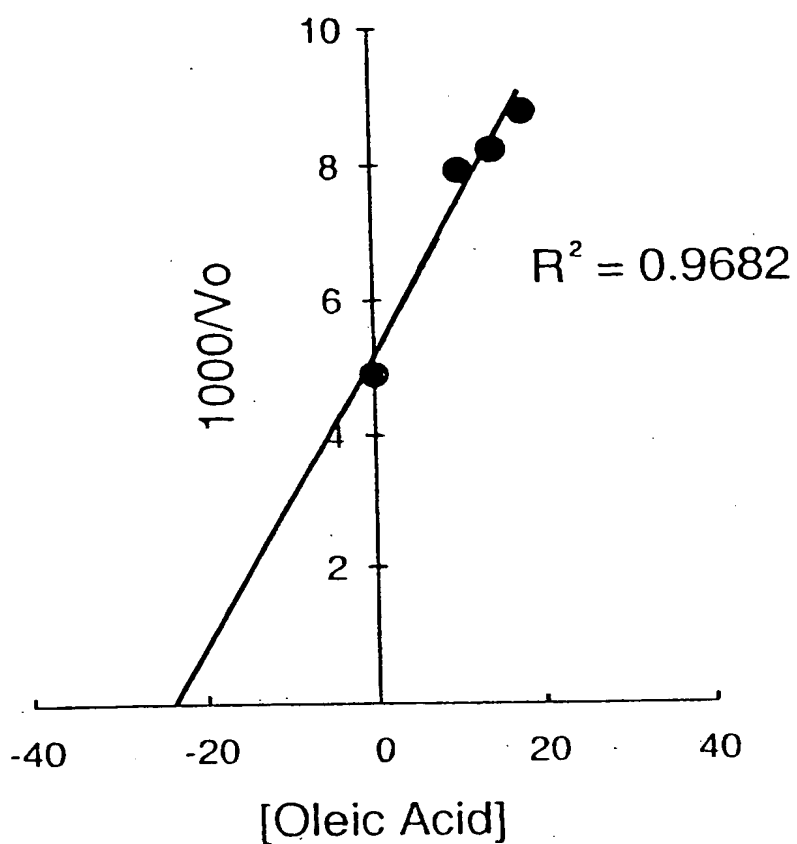
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Effect of oleic acid on isomerase activity with linoleic acid as substrate. The concentration of linoleic acid was fixed at 36 μ M. Oleic acid was added at the indicated concentrations.

FIG. 47

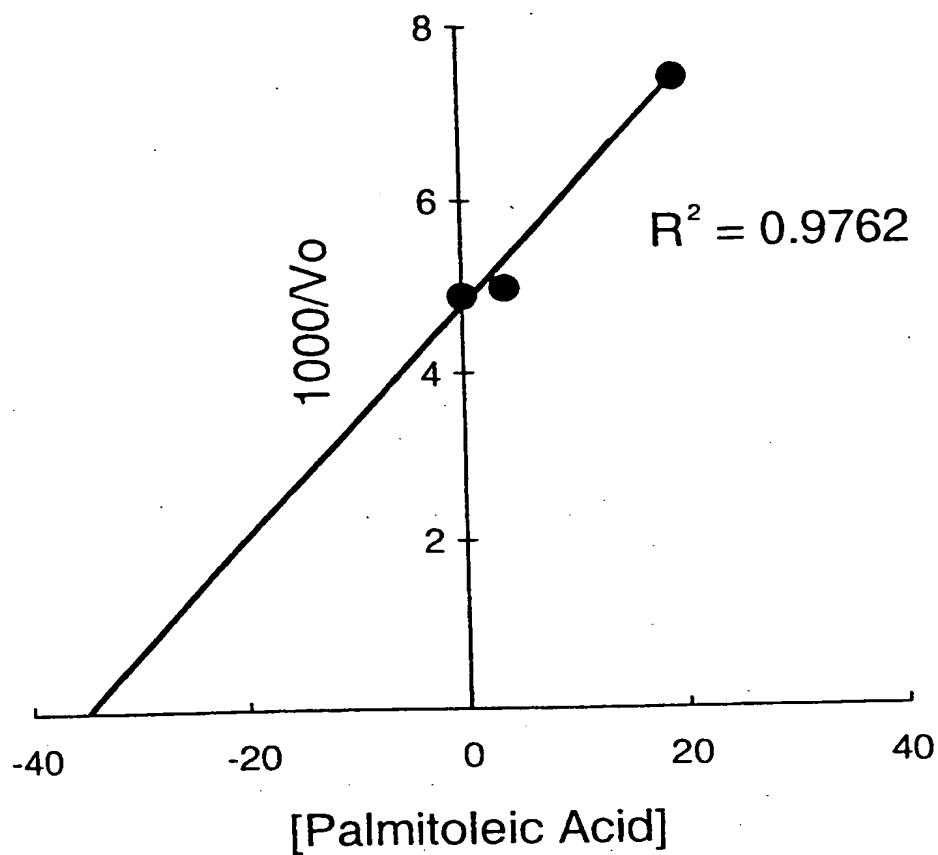
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Secondary plot of oleic acid inhibition. V_o as nmols
CLA/min/mg protein. $[Oleic\ Acid]$ as μM

FIG. 48

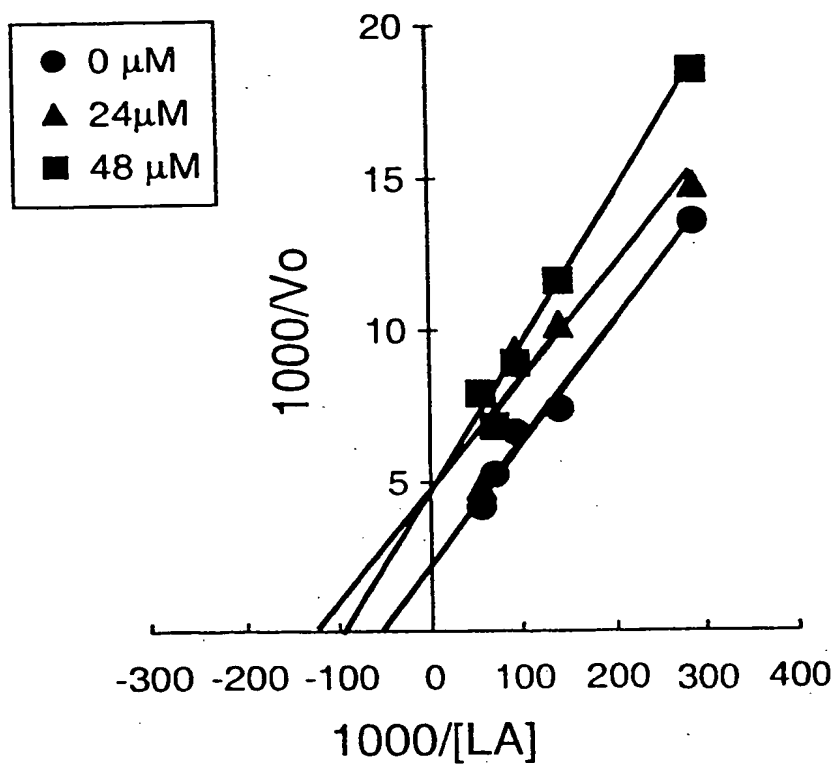
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Secondary plot of palmitoleic acid-inhibition: V_o as nmols
CLA/min/mg protein. $[Palmitoleic\ Acid]$ as μM

FIG. 49

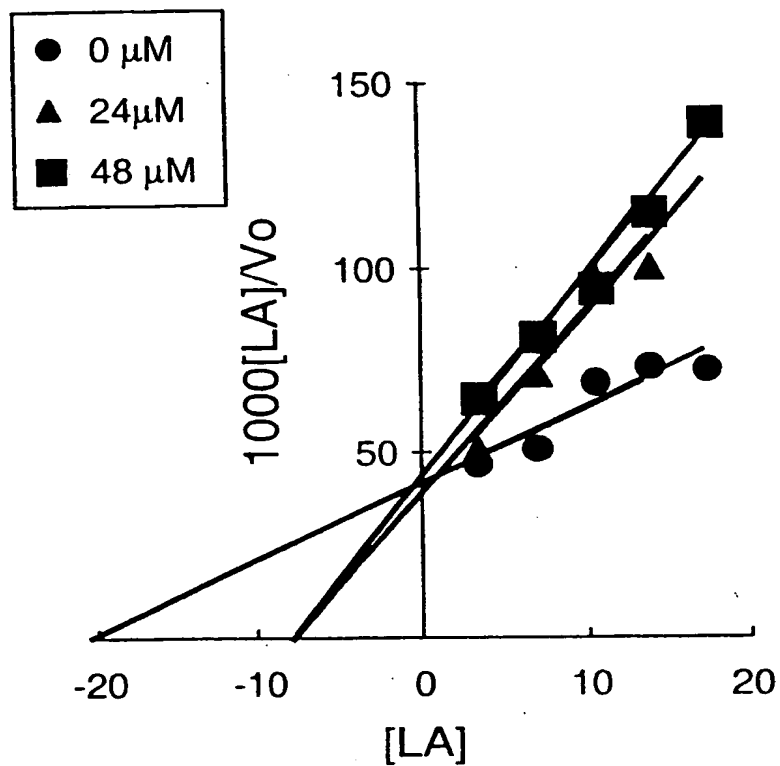
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Lineweaver-Burk plot of linoleic acid isomerization kinetics in the presence or absence of oleic acid.
 V_o as nmols CLA/min/mg protein. $[LA]$ as μM .

FIG. 50

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Hanes-Woolf plot of oleic acid inhibition of linoleic acid isomerization kinetics. V_o as nmols CLA/min/mg protein. $[LA]$ as μM .

FIG. 51

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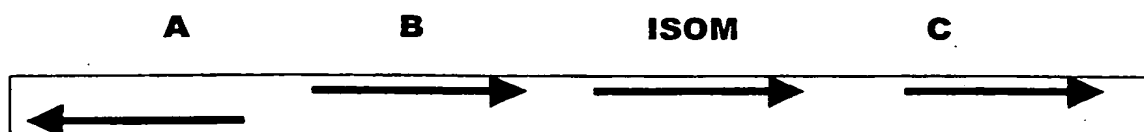


FIG. 52

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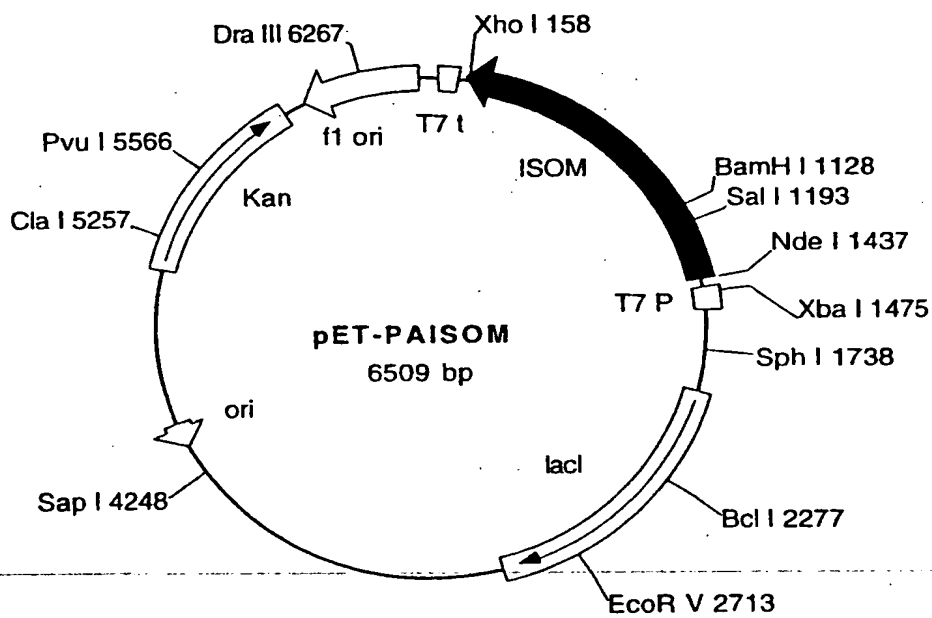


FIG. 53

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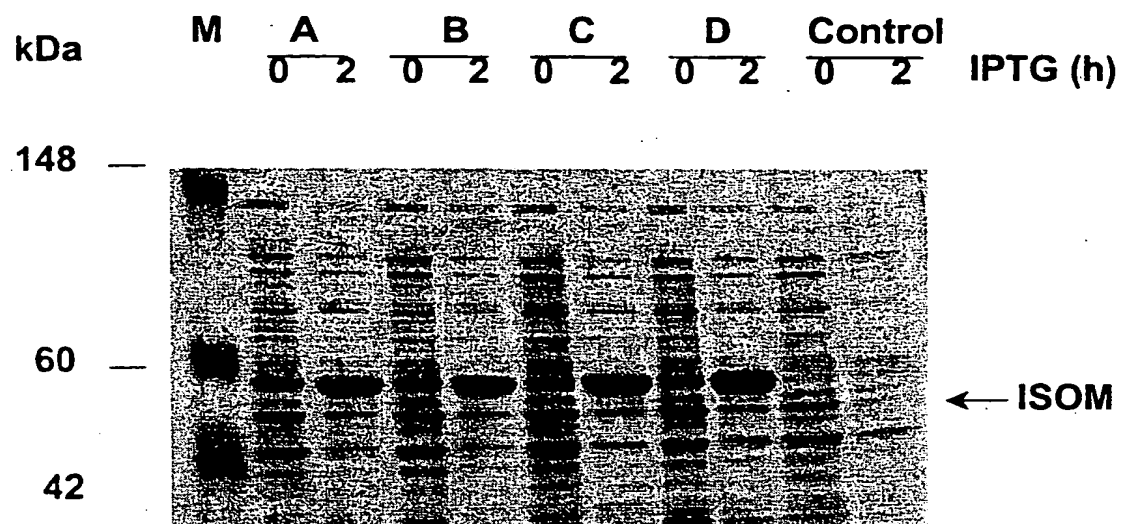


FIG. 54

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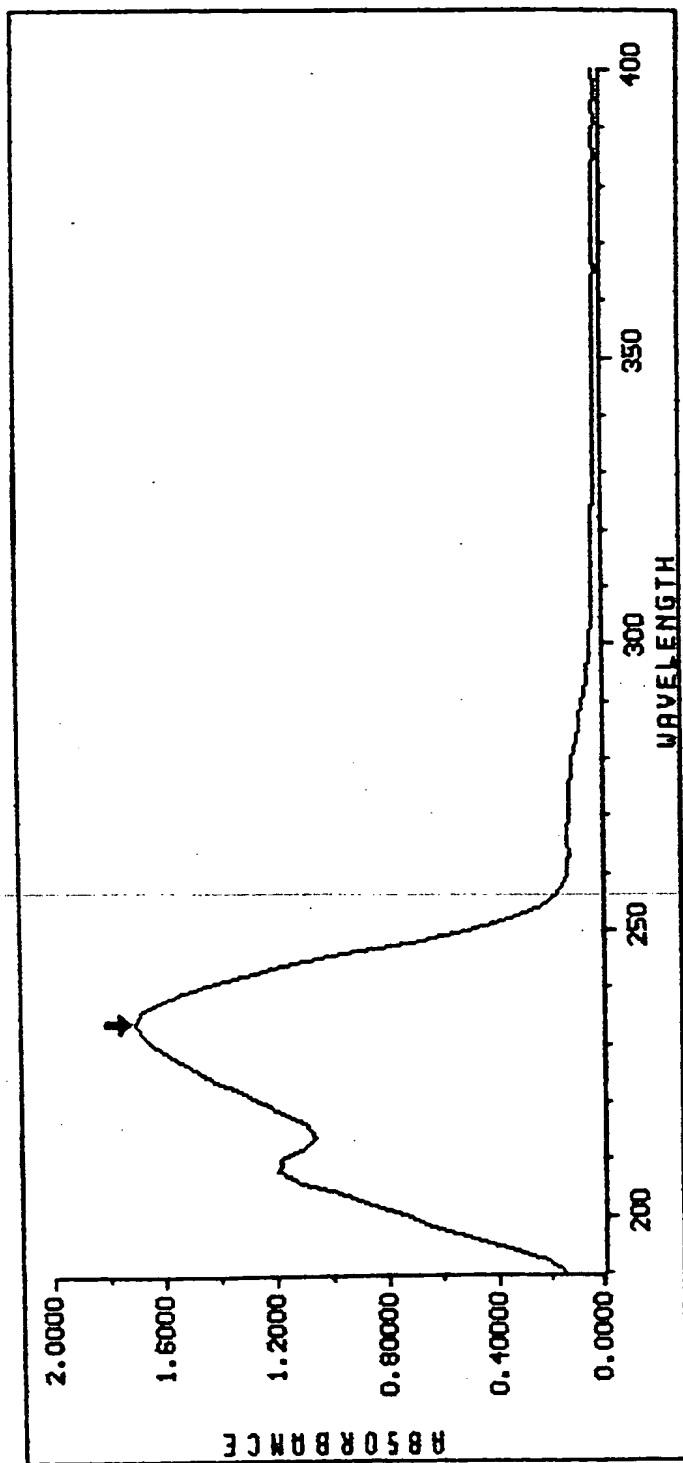


FIG. 55

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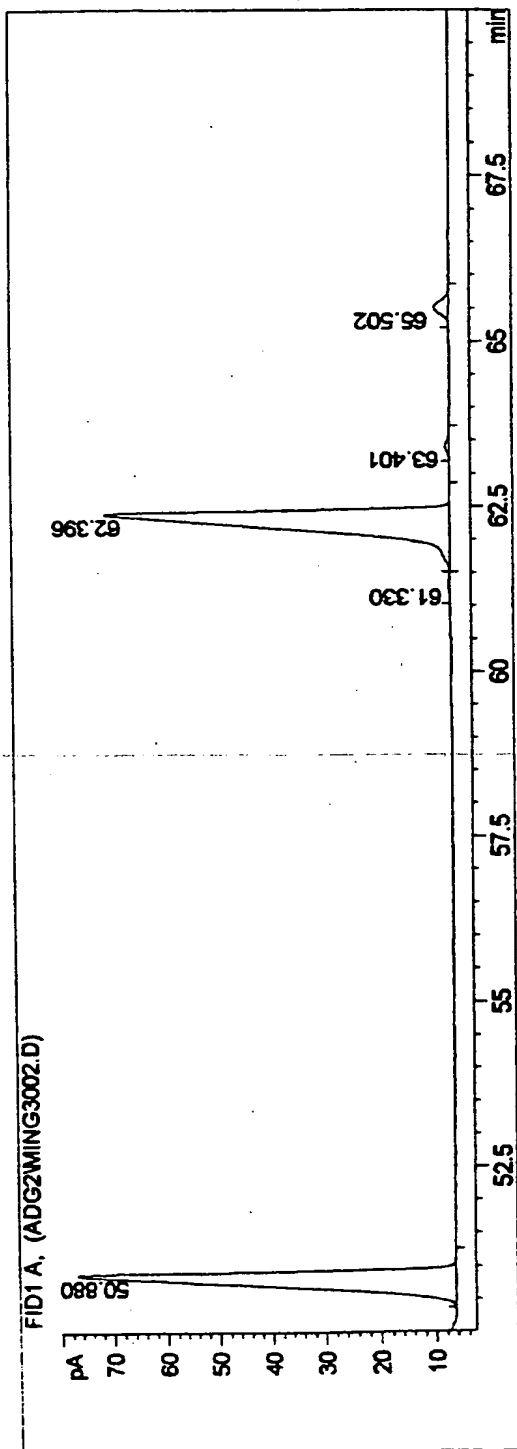


FIG. 56A

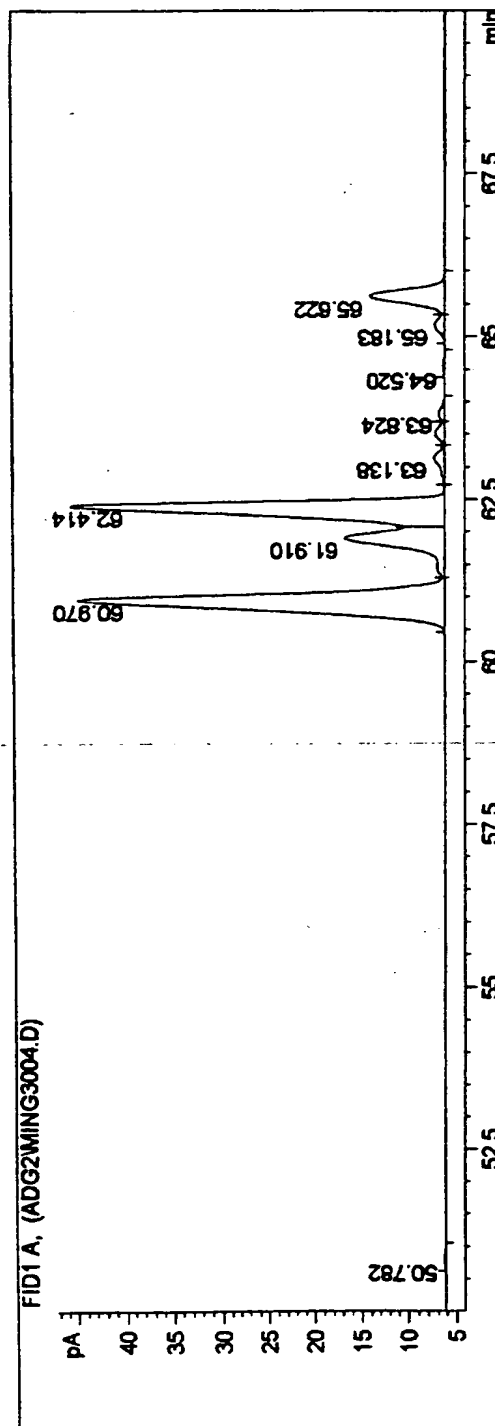


FIG. 56B

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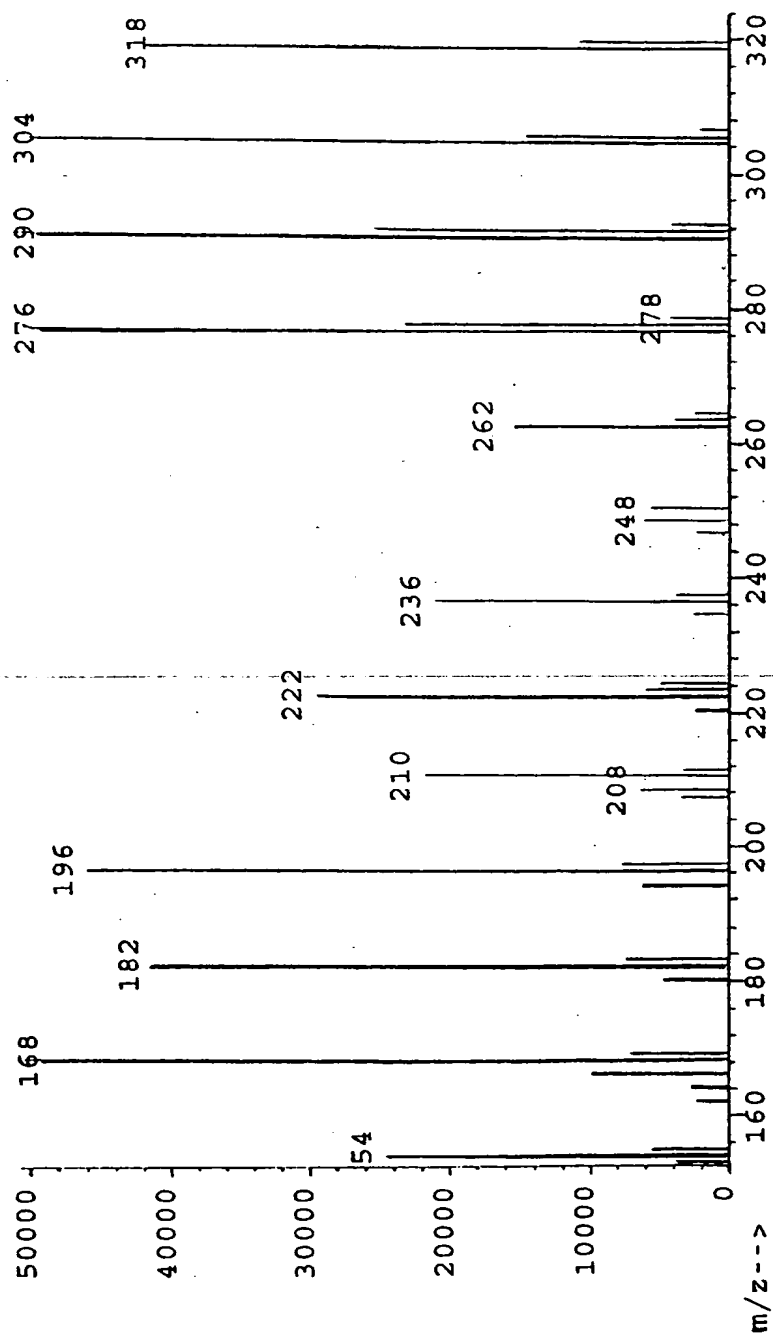
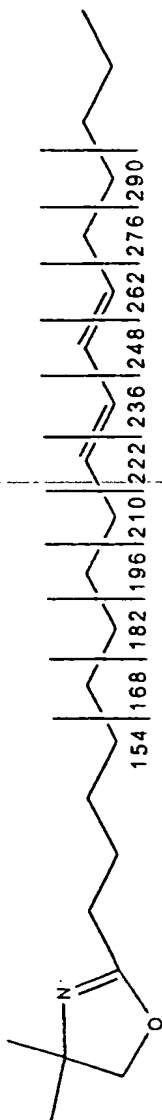


FIG. 57

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A putative NAD-binding domain shared by linoleate isomerases and some other enzymes

NAD-binding domain

CONSENSUS	G-G-G-A-L-----G-----E-----GG-----G-----G	(SEQ ID NO:73)
#1 183 SEAYSAKIALF*A*PASISC*SF*-----ARL*YSDITIF*KQEVV**		(SEQ ID NO:74)
#2 8 KVAIV*A*LS*LVV*SE*-----LHA*IDDVITY*ASDRI**KLMS		(SEQ ID NO:75)
#3 140 VKTGKKVAVV*S*PA*LAA*QQ*-----ARA*-HDVTVF*KNDRV**RIEQ		(SEQ ID NO:76)
#4 6 VV*G*FS*LKA*RD*-----TNA*-KKVLL*GGERL**RAYS		(SEQ ID NO:77)
#5 8 RIAII*A*LA*MAT*VE*-----VDA*-HEVELY*ARSEFI**KVGSWVDGD*NHI-EM*		(SEQ ID NO:78)
#6 3 STSKRPTAIVI*S*VG*VST*AR*-----ARA*FH-VTVL*KNNFT**RCSL-IHHE*YRF-DQ*		(SEQ ID NO:79)
#7 8 RVIVV*A*MS*ISA*KR*-----SEA*ITDLLIL*ATDHI**RMHK-TNFA*INV-EL*		(SEQ ID NO:80)
#8 2 SISKDSRIALL*A*PA*LAAGMY*-----EQA*FHDYITIL*RTDHF**KCHS-PNYH*RRY-EM*		(POS. 2-59 OF SEQ ID NO:61)
#9 19 GVDKK-HAYIV*G*LA*LSA*VF*IRDAQMP*-ENIHIL*ELPVA**SLDG-EDRF*IGFVTR*		(POS. 19-79 OF SEQ ID NO:18)

SEQUENCE ORIGIN:

- #1: Dihydropyrimidine dehydrogenase (Human), Q12882
 #2: Tryptophane monooxygenase (Agrobacterium vitis), AAC77909.1
 #3: Glutamate synthase (Deinococcus radiodurans), AAF09769.1
 #4: 6-hydroxy-L-nicotine oxidase (Arthrobacter nicotinovorans), AJ223391
 #5: ζ-Caroten desaturase (Synechocystis sp.), D90914
 #6: Phytoene dehydrogenase (Cercospora nicotianae), P48537
 #7: Polyamine oxidase (Zea mays), O64411
 #8: (t, c)-10,12-Linoleate isomerase (Propionibacterium acnes)
 #9: (c, t)-9,11-Linoleate isomerase (Lactobacillus reuteri)

FIG. 58

SEQUENCE LISTING

<110> Rosson, Reinhardt D.
Deng, Ming-de
Grund, Alan D.
Peng, Susan

<120> LINOLEATE ISOMERASE

<130> 3161-20-cl-pct

<140> Not Yet Assigned

<141> 2000-06-30

<150> 60/141,798

<151> 1999-06-30

<150> 09/561,077

<151> 2000-04-28

<160> 82

<170> PatentIn Ver. 2.1

<210> 1

<211> 35

<212> PRT

<213> Lactobacillus reuteri

<220>

<221> UNSURE

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Met	Tyr	Tyr	Ser	Asn	Gly	Asn	Tyr	Glu	Ala	Phe	Ala	Arg	Pro	Lys	Lys
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Pro	Ala	Gly	Val	Asp	Lys	Lys	His	Ala	Tyr	Ile	Val	Gly	Xaa	Gly	Leu
			20					25						30	

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Met	Tyr	Tyr	Ser	Asn	Gly	Asn	Tyr	Glu	Ala	Phe	Ala	Arg	Pro	Lys	Lys	
1				5				10						15		

cct	gct	ggc	gtt	gat	aag	aaa	cac	gcc	tac	ata	gtc	gga	87
Pro	Ala	Gly	Val	Asp	Lys	Lys	His	Ala	Tyr	Ile	Val	Gly	
			20					25					

<210> 5

<211> 29

<212> PRT

<213> Lactobacillus reuteri

<400> 5

Met	Tyr	Tyr	Ser	Asn	Gly	Asn	Tyr	Glu	Ala	Phe	Ala	Arg	Pro	Lys	Lys
1				5				10						15	

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 <213> Lactobacillus reuteri

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17

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17

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 Met Tyr Tyr Ser Asn Gly Asn Tyr Glu Ala Phe Ala Arg Pro Lys Lys
 1 5 10 15
 cct gct ggc gtt gat aag aaa cat gcc tac att gtc ggt ggt ggt tta 217
 Pro Ala Gly Val Asp Lys Lys His Ala Tyr Ile Val Gly Gly Gly Leu
 20 25 30
 gct ggt tta tcg gcc gcc gtg ttt tta att cgt gat gcc caa atg ccg 265
 Ala Gly Leu Ser Ala Ala Val Phe Leu Ile Arg Asp Ala Gln Met Pro
 35 40 45
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 Gly Glu Asn Ile His Ile Leu Glu Glu Leu Pro Val Ala Gly Gly Ser
 50 55 60
 ctt gat ggt gaa gat cgt cct gga att ggt ttt gtt act cgt gga ggc 361

Leu Asp Gly Glu Asp Arg Pro Gly Ile Gly Phe Val Thr Arg Gly Gly
 65 70 75 80
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 Arg Glu Met Glu Asn His Phe Glu Cys Met Trp Asp Met Tyr Arg Ser
 85 90 95
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 Ile Pro Ser Leu Glu Ile Pro Gly Ala Ser Tyr Leu Asp Glu Tyr Tyr
 100 105 110
 tgg tta gat aag gaa gat cca aac agt tct aat tgt cgt tta acc tat 505
 Trp Leu Asp Lys Glu Asp Pro Asn Ser Ser Asn Cys Arg Leu Thr Tyr
 115 120 125
 aag cgg gga aat gaa gtt cca tcg gac ggt aaa tat ggt tta agt aaa 553
 Lys Arg Gly Asn Glu Val Pro Ser Asp Gly Lys Tyr Gly Leu Ser Lys
 130 135 140
 aag gca atc aaa gag ctg act aag cta att atg acc cct aaa g 596
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<210> 9

<211> 158

<212> PRT

<213> Lactobacillus reuteri

<400> 9

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 35 40 45
 Gly Glu Asn Ile His Ile Leu Glu Glu Leu Pro Val Ala Gly Gly Ser
 50 55 60
 Leu Asp Gly Glu Asp Arg Pro Gly Ile Gly Phe Val Thr Arg Gly Gly
 65 70 75 80
 Arg Glu Met Glu Asn His Phe Glu Cys Met Trp Asp Met Tyr Arg Ser
 85 90 95

Ile Pro Ser Leu Glu Ile Pro Gly Ala Ser Tyr Leu Asp Glu Tyr Tyr
 100 105 110

Trp Leu Asp Lys Glu Asp Pro Asn Ser Ser Asn Cys Arg Leu Thr Tyr
 115 120 125

Lys Arg Gly Asn Glu Val Pro Ser Asp Gly Lys Tyr Gly Leu Ser Lys
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Lys Ala Ile Lys Glu Leu Thr Lys Leu Ile Met Thr Pro Lys
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<211> 1709

<212> DNA

<213> *Lactobacillus reuteri*

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1709

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<211> 324

<212> PRT

<213> Lactobacillus reuteri

<220>

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<222> (315)

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Ala Gly Leu Ser Ala Ala Val Phe Leu Ile Arg Asp Ala Gln Met Pro
35 40 45

Gly Glu Asn Ile His Ile Leu Glu Glu Leu Pro Val Ala Gly Gly Ser
50 55 60

Leu Asp Gly Glu Asp Arg Pro Gly Ile Gly Phe Val Thr Arg Gly Gly
65 70 75 80

Arg Glu Met Glu Asn His Phe Glu Cys Met Trp Asp Met Tyr Arg Ser
85 90 95

Ile Pro Ser Leu Glu Ile Pro Gly Ala Ser Tyr Leu Asp Glu Tyr Tyr
100 105 110

Trp Leu Asp Lys Glu Asp Pro Asn Ser Ser Asn Cys Arg Leu Thr Tyr
115 120 125

Lys Arg Gly Asn Glu Val Pro Ser Asp Gly Lys Tyr Gly Leu Ser Lys
130 135 140

Lys Ala Ile Lys Glu Leu Thr Lys Leu Ile Met Thr Pro Glu Glu Lys
145 150 155 160

Leu Gly Arg Glu Thr Ile Gly Glu Tyr Phe Ser Asp Asp Phe Phe Glu
165 170 175

Ser Asn Phe Trp Ile Tyr Trp Ser Thr Met Phe Ala Phe Glu Arg Trp
180 185 190

His Ser Leu Ala Glu Met Arg Arg Tyr Met Met Arg Phe Ile His His
 195 200 205

Ile Asp Gly Leu Pro Asp Phe Thr Ala Leu Lys Phe Asn Lys Tyr Asn
 210 215 220

Gln Tyr Glu Ser Met Thr Lys Pro Leu Leu Ala Tyr Leu Lys Asp His
 225 230 235 240

His Val Lys Ile Glu Tyr Asp Thr Gln Val Lys Asn Val Ile Val Asp
 245 250 255

Thr His Gly Arg Gln Lys His Ala Lys Arg Ile Leu Leu Thr Gln Ala
 260 265 270

Gly Lys Asp Lys Val Val Glu Leu Thr Asp Asn Asp Leu Val Phe Val
 275 280 285

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Lys Pro Cys Ser

<210> 12

<211> 17

<212> DNA

<213> Lactobacillus reuteri

<400> 12

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17

<210> 13

<211> 19

<212> DNA

<213> Lactobacillus reuteri

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19

<210> 14

<211> 1165

<212> DNA

<213> *Lactobacillus reuteri*

<400> 14

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<210> 15

<211> 2319

<212> DNA

<213> *Lactobacillus reuteri*

<400> 15

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<210> 16

<211> 3551

<212> DNA

<213> *Lactobacillus reuteri*

<400> 16

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<210> 17

<211> 1776

<212> DNA

<213> *Lactobacillus reuteri*

<220>

<221> CDS

<222> (1)..(1776)

<400> 17

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Pro Ala Gly Val Asp Lys Lys His Ala Tyr Ile Val Gly Gly Gly Leu	
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gct ggt tta tcg gcc gcc gtg ttt tta att cgt gat gcc caa atg ccg	144
Ala Gly Leu Ser Ala Ala Val Phe Leu Ile Arg Asp Ala Gln Met Pro	
35 40 45	
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Gly Glu Asn Ile His Ile Leu Glu Glu Leu Pro Val Ala Gly Gly Ser	
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Leu Asp Gly Glu Asp Arg Pro Gly Ile Gly Phe Val Thr Arg Gly Gly	
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Arg Glu Met Glu Asn His Phe Glu Cys Met Trp Asp Met Tyr Arg Ser	
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Ile Pro Ser Leu Glu Ile Pro Gly Ala Ser Tyr Leu Asp Glu Tyr Tyr	
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Ile Asp Gly Leu Pro Asp Phe Thr Ala Leu Lys Phe Asn Lys Tyr Asn	
210 215 220	
caa tat gaa tca atg acc aag ccg cta ttg gcc tac ctg aaa gat cat	720
Gln Tyr Glu Ser Met Thr Lys Pro Leu Leu Ala Tyr Leu Lys Asp His	
225 230 235 240	
cat gtc aag att gag tac gat acc cag gta aag aat gtt att gtt gat	768
His Val Lys Ile Glu Tyr Asp Thr Gln Val Lys Asn Val Ile Val Asp	
245 250 255	
act cat ggg cgg caa aag cac gct aag cga atc tta tta act caa gcc	816
Thr His Gly Arg Gln Lys His Ala Lys Arg Ile Leu Leu Thr Gln Ala	
260 265 270	
ggt aaa gat aaa gtt gtt gag tta acg gac aat gac ctt gtc ttt gtc	864
Gly Lys Asp Lys Val Val Glu Leu Thr Asp Asn Asp Leu Val Phe Val	
275 280 285	
aca aac ggt tca att aca gaa agt tct act tac ggc agt cac cat caa	912
Thr Asn Gly Ser Ile Thr Glu Ser Ser Thr Tyr Gly Ser His His Gln	
290 295 300	
gca gct cga cca acg caa gca ctt ggt ggt agt tgg aaa ctg tgg gaa	960
Ala Ala Arg Pro Thr Gln Ala Leu Gly Gly Ser Trp Lys Leu Trp Glu	
305 310 315 320	
aac ctt gct cgg cag tca gct gat ttt ggt cat cct gat gtc ttt tgc	1008
Asn Leu Ala Arg Gln Ser Ala Asp Phe Gly His Pro Asp Val Phe Cys	
325 330 335	
aag aat ctt cca ggg aga agc tgg ttc att tcc gct act gca acc gtt	1056
Lys Asn Leu Pro Gly Arg Ser Trp Phe Ile Ser Ala Thr Ala Thr Val	
340 345 350	

aag aac ccg caa gtt gaa cca tac att gaa cgc tta acc aag cga gat	1104
Lys Asn Pro Gln Val Glu Pro Tyr Ile Glu Arg Leu Thr Lys Arg Asp	
355 360 365	
ctc cat gat ggc aaa gtt aat act ggt gga atc att acg gtc act gac	1152
Leu His Asp Gly Lys Val Asn Thr Gly Gly Ile Ile Thr Val Thr Asp	
370 375 380	
tct aat tgg atg ctt tcc tgg aca att cac cgt caa ccg cac ttc aag	1200
Ser Asn Trp Met Leu Ser Trp Thr Ile His Arg Gln Pro His Phe Lys	
385 390 395 400	
aaa caa aag aaa aat gaa acc att gtt tgg att tac ggt ctg tac tct	1248
Lys Gln Lys Lys Asn Glu Thr Ile Val Trp Ile Tyr Gly Leu Tyr Ser	
405 410 415	
aat aca aag gga aac tat att aag aaa cgg atc gtt gat tgt act ggt	1296
Asn Thr Lys Gly Asn Tyr Ile Lys Lys Arg Ile Val Asp Cys Thr Gly	
420 425 430	
gaa gag att act aaa gaa tgg cta tcc atc tgg ggg ttc cag aag ccg	1344
Glu Glu Ile Thr Lys Glu Trp Leu Ser Ile Trp Gly Phe Gln Lys Pro	
435 440 445	
tta att gac gat ttg gct aag gag agt tca att aat act gtt cca gta	1392
Leu Ile Asp Asp Leu Ala Lys Glu Ser Ser Ile Asn Thr Val Pro Val	
450 455 460	
tat atg cca ttt atc act agc tac ttt atg cca cga gtt aag ggc gac	1440
Tyr Met Pro Phe Ile Thr Ser Tyr Phe Met Pro Arg Val Lys Gly Asp	
465 470 475 480	
cgt cca gac gtt gtt cca gaa gga tcc gct aac ttg gca ttt att ggt	1488
Arg Pro Asp Val Val Pro Glu Gly Ser Ala Asn Leu Ala Phe Ile Gly	
485 490 495	
aac ttt gct gaa tct cca agt cga gat acc gta ttt acc acg gaa tat	1536
Asn Phe Ala Glu Ser Pro Ser Arg Asp Thr Val Phe Thr Thr Glu Tyr	
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Ser Val Arg Thr Ala Met Glu Ala Val Tyr Thr Leu Leu Asp Val Asp	
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Arg Gly Val Pro Glu Val Phe Asn Ser Ile Tyr Asp Leu Arg Glu Leu	
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atg cgg gca atg tat tac atg aat gat aag aag ccg tta aaa gac atg 1680
 Met Arg Ala Met Tyr Tyr Met Asn Asp Lys Lys Pro Leu Lys Asp Met
 545 550 555 560

gac ttg cca att cca aag att gtt gaa aag cca tta tta aag aaa ctc 1728
 Asp Leu Pro Ile Pro Lys Ile Val Glu Lys Pro Leu Leu Lys Lys Leu
 565 570 575

caa gga acg tgg att ggt gaa tta atg gag caa cag cac tta cta taa 1776
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<211> 591

<212> PRT

<213> Lactobacillus reuteri

<400> 18

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 35 40 45
 Gly Glu Asn Ile His Ile Leu Glu Glu Leu Pro Val Ala Gly Gly Ser
 50 55 60
 Leu Asp Gly Glu Asp Arg Pro Gly Ile Gly Phe Val Thr Arg Gly Gly
 65 70 75 80
 Arg Glu Met Glu Asn His Phe Glu Cys Met Trp Asp Met Tyr Arg Ser
 85 90 95
 Ile Pro Ser Leu Glu Ile Pro Gly Ala Ser Tyr Leu Asp Glu Tyr Tyr
 100 105 110
 Trp Leu Asp Lys Glu Asp Pro Asn Ser Ser Asn Cys Arg Leu Thr Tyr
 115 120 125
 Lys Arg Gly Asn Glu Val Pro Ser Asp Gly Lys Tyr Gly Leu Ser Lys
 130 135 140
 Lys Ala Ile Lys Glu Leu Thr Lys Leu Ile Met Thr Pro Glu Glu Lys
 145 150 155 160
 Leu Gly Arg Glu Thr Ile Gly Glu Tyr Phe Ser Asp Asp Phe Phe Glu
 165 170 175
 Ser Asn Phe Trp Ile Tyr Trp Ser Thr Met Phe Ala Phe Glu Arg Trp
 180 185 190
 His Ser Leu Ala Glu Met Arg Arg Tyr Met Met Arg Phe Ile His His
 195 200 205
 Ile Asp Gly Leu Pro Asp Phe Thr Ala Leu Lys Phe Asn Lys Tyr Asn
 210 215 220
 Gln Tyr Glu Ser Met Thr Lys Pro Leu Leu Ala Tyr Leu Lys Asp His

225	230	235	240
His Val Lys Ile Glu Tyr Asp Thr Gln Val Lys Asn Val Ile Val Asp			
	245	250	255
Thr His Gly Arg Gln Lys His Ala Lys Arg Ile Leu Leu Thr Gln Ala			
	260	265	270
Gly Lys Asp Lys Val Val Glu Leu Thr Asp Asn Asp Leu Val Phe Val			
	275	280	285
Thr Asn Gly Ser Ile Thr Glu Ser Ser Thr Tyr Gly Ser His His Gln			
	290	295	300
Ala Ala Arg Pro Thr Gln Ala Leu Gly Gly Ser Trp Lys Leu Trp Glu			
305	310	315	320
Asn Leu Ala Arg Gln Ser Ala Asp Phe Gly His Pro Asp Val Phe Cys			
	325	330	335
Lys Asn Leu Pro Gly Arg Ser Trp Phe Ile Ser Ala Thr Ala Thr Val			
	340	345	350
Lys Asn Pro Gln Val Glu Pro Tyr Ile Glu Arg Leu Thr Lys Arg Asp			
	355	360	365
Leu His Asp Gly Lys Val Asn Thr Gly Gly Ile Ile Thr Val Thr Asp			
	370	375	380
Ser Asn Trp Met Leu Ser Trp Thr Ile His Arg Gln Pro His Phe Lys			
385	390	395	400
Lys Gln Lys Lys Asn Glu Thr Ile Val Trp Ile Tyr Gly Leu Tyr Ser			
	405	410	415
Asn Thr Lys Gly Asn Tyr Ile Lys Lys Arg Ile Val Asp Cys Thr Gly			
	420	425	430
Glu Glu Ile Thr Lys Glu Trp Leu Ser Ile Trp Gly Phe Gln Lys Pro			
	435	440	445
Leu Ile Asp Asp Leu Ala Lys Glu Ser Ser Ile Asn Thr Val Pro Val			
	450	455	460
Tyr Met Pro Phe Ile Thr Ser Tyr Phe Met Pro Arg Val Lys Gly Asp			
465	470	475	480
Arg Pro Asp Val Val Pro Glu Gly Ser Ala Asn Leu Ala Phe Ile Gly			
	485	490	495
Asn Phe Ala Glu Ser Pro Ser Arg Asp Thr Val Phe Thr Thr Glu Tyr			
	500	505	510
Ser Val Arg Thr Ala Met Glu Ala Val Tyr Thr Leu Leu Asp Val Asp			
	515	520	525
Arg Gly Val Pro Glu Val Phe Asn Ser Ile Tyr Asp Leu Arg Glu Leu			
	530	535	540
Met Arg Ala Met Tyr Tyr Met Asn Asp Lys Lys Pro Leu Lys Asp Met			
545	550	555	560
Asp Leu Pro Ile Pro Lys Ile Val Glu Lys Pro Leu Leu Lys Lys Leu			
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Gln Gly Thr Trp Ile Gly Glu Leu Met Glu Gln Gln His Leu Leu			
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gat ggt caa gaa aca cca cca tta aag atc cat caa tta ttt gat tca 96
 Asp Gly Gln Glu Thr Pro Pro Leu Lys Ile His Gln Leu Phe Asp Ser
 20 25 30

caa aaa tac gat cag tta atc gca gta act ggg aaa att act gct gac 144
 Gln Lys Tyr Asp Gln Leu Ile Ala Val Thr Gly Lys Ile Thr Ala Asp
 35 40 45

ttc att aat aaa tac ctt agt aat ttt atc agt att aat gta gcg tta 192
 Phe Ile Asn Lys Tyr Leu Ser Asn Phe Ile Ser Ile Asn Val Ala Leu
 50 55 60

agc tcc caa tca act agt gaa tta agt gct gat gag atg gtg aca aag 240
 Ser Ser Gln Ser Thr Ser Glu Leu Ser Ala Asp Glu Met Val Thr Lys
 65 70 75 80

gtt gca ctt acc aat gct ctc ctt agt tca gca aat aaa gaa gct gct 288
 Val Ala Leu Thr Asn Ala Leu Leu Ser Ser Ala Asn Lys Glu Ala Ala
 85 90 95

aaa ctc ttc tca gcg tta acc agt gac aac caa acg aac gtc tta aat 336
 Lys Leu Phe Ser Ala Leu Thr Ser Asp Asn Gln Thr Asn Val Leu Asn
 100 105 110

aat ctt ttt cgc gta tca atc gcg cct act cag gtt atc cat tct aag 384
 Asn Leu Phe Arg Val Ser Ile Ala Pro Thr Gln Val Ile His Ser Lys
 115 120 125

ttt tac ttg tta agt agt tca act act cat gat tcc cgt gtg att ctt 432
 Phe Tyr Leu Leu Ser Ser Thr Thr His Asp Ser Arg Val Ile Leu
 130 135 140

ggg agt gta gat tta gac gaa gct tca ttt gat gct cac cga aat caa 480
 Gly Ser Val Asp Leu Asp Glu Ala Ser Phe Asp Ala His Arg Asn Gln

145	150	155	160	
ttt gaa gaa gta ttg gta ttt gac aat gat gtc cgc tta tac caa aac				528
Phe Glu Glu Val Leu Val Phe Asp Asn Asp Val Arg Leu Tyr Gln Asn				
	165	170	175	
ctt act gac cac ttt aaa aag gat ttt aag cca gta ttg aag ccc ttc				576
Leu Thr Asp His Phe Lys Lys Asp Phe Lys Pro Val Leu Lys Pro Phe				
	180	185	190	
ttt act atg aac cta gta aag gca gct caa aag caa gtt gag gaa gga				624
Phe Thr Met Asn Leu Val Lys Ala Ala Gln Lys Gln Val Glu Glu Gly				
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Lys Lys Asp Gln Asp Ser Gly Lys Gly Pro				
	210	215		

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<211> 218

<212> PRT

<213> Lactobacillus reuteri

<400> 20

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	20	25	30
Gln Lys Tyr Asp Gln Leu Ile Ala Val Thr Gly Lys Ile Thr Ala Asp			
	35	40	45
Phe Ile Asn Lys Tyr Leu Ser Asn Phe Ile Ser Ile Asn Val Ala Leu			
	50	55	60
Ser Ser Gln Ser Thr Ser Glu Leu Ser Ala Asp Glu Met Val Thr Lys			
	65	70	75
Val Ala Leu Thr Asn Ala Leu Leu Ser Ser Ala Asn Lys Glu Ala Ala			
	85	90	95
Lys Leu Phe Ser Ala Leu Thr Ser Asp Asn Gln Thr Asn Val Leu Asn			
	100	105	110
Asn Leu Phe Arg Val Ser Ile Ala Pro Thr Gln Val Ile His Ser Lys			
	115	120	125

Phe Tyr Leu Leu Ser Ser Ser Thr Thr His Asp Ser Arg Val Ile Leu
130 135 140

Gly Ser Val Asp Leu Asp Glu Ala Ser Phe Asp Ala His Arg Asn Gln
145 150 155 160

Phe Glu Glu Val Leu Val Phe Asp Asn Asp Val Arg Leu Tyr Gln Asn
165 170 175

Leu Thr Asp His Phe Lys Lys Asp Phe Lys Pro Val Leu Lys Pro Phe
180 185 190

Phe Thr Met Asn Leu Val Lys Ala Ala Gln Lys Gln Val Glu Glu Gly
195 200 205

Lys Lys Asp Gln Asp Ser Gly Lys Gly Pro
210 215

<210> 21

<211> 726

<212> DNA

<213> Lactobacillus reuteri

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<220>

<221> unsure

<222> (12)

<220>

<221> unsure

<222> (297)

<220>

<221> misc_feature

<222> (10)..(12)

<223> Xaa = Tyr or stop

<220>

<221> misc_feature

<222> (295)..(297)

<223> Xaa = Tyr or stop

<400> 21

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gtc aca acg atc aaa aaa aca tta ccg cca act cag gaa cag gct aat	96
Val Thr Thr Ile Lys Lys Thr Leu Pro Pro Thr Gln Glu Gln Ala Asn	
20 25 30	
tca gtc tta act ccg gct gtt cgc caa caa ctt ggc att tca att acc	144
Ser Val Leu Thr Pro Ala Val Arg Gln Gln Leu Gly Ile Ser Ile Thr	
35 40 45	
tgg aac aaa gcc ggt gcg ttt att atc aat aat aac caa aca aat ctt	192
Trp Asn Lys Ala Gly Ala Phe Ile Ile Asn Asn Asn Gln Thr Asn Leu	
50 55 60	
aac gct aag att gca agt gca ccc tat gct gta aat cat ctt gac cgt	240
Asn Ala Lys Ile Ala Ser Ala Pro Tyr Ala Val Asn His Leu Asp Arg	
65 70 75 80	
caa gga agg gcg tgg caa ggt gat gcc tgg tta aac agg aca act cgg	288
Gln Gly Arg Ala Trp Gln Gly Asp Ala Trp Leu Asn Arg Thr Thr Arg	
85 90 95	
tca ata tan aag ccg aaa ttt gcc aca ggg aat ggt gct acg gat tgg	336
Ser Ile Xaa Lys Pro Lys Phe Ala Thr Gly Asn Gly Ala Thr Asp Trp	
100 105 110	
cga cca gct ggc ttc ctt cag gcg cat aat ctt aaa ggc ggg tac aat	384
Arg Pro Ala Gly Phe Leu Gln Ala His Asn Leu Lys Gly Gly Tyr Asn	
115 120 125	
cat gca tac gat cgc gga cac ctt ctt gcc tat gca cta gtt ggt ggt	432
His Ala Tyr Asp Arg Gly His Leu Leu Ala Tyr Ala Leu Val Gly Gly	
130 135 140	
att cat gga ttt gat gca tcc gaa tca aat cca tct aat att gcc acg	480
Ile His Gly Phe Asp Ala Ser Glu Ser Asn Pro Ser Asn Ile Ala Thr	
145 150 155 160	
caa act gcc tgg gca aat gaa gca cga agt aag aac tca aca ggg caa	528
Gln Thr Ala Trp Ala Asn Glu Ala Arg Ser Lys Asn Ser Thr Gly Gln	
165 170 175	
aat tac tac gaa ggt ctg gtg aga aaa gca tta gat cag aat aag caa	576
Asn Tyr Tyr Glu Gly Leu Val Arg Lys Ala Leu Asp Gln Asn Lys Gln	
180 185 190	

gtt cgc tac cga gtt acc aat att tat gac ggt aat aat atc gtt ccg 624
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 195 200 205

gca ggt gct cat atc gaa gct aaa tct agt gat ggt tct cta gaa tac 672
 Ala Gly Ala His Ile Glu Ala Lys Ser Ser Asp Gly Ser Leu Glu Tyr
 210 215 220

aat gtc ttt gtt ccg aat gtc caa aga aac att acc att aat tat tca 720
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acc ggt 726
 Thr Gly

<210> 22

<211> 242

<212> PRT

<213> Lactobacillus reuteri

<400> 22

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 35 40 45

Trp Asn Lys Ala Gly Ala Phe Ile Ile Asn Asn Asn Gln Thr Asn Leu
 50 55 60

Asn Ala Lys Ile Ala Ser Ala Pro Tyr Ala Val Asn His Leu Asp Arg
 65 70 75 80

Gln Gly Arg Ala Trp Gln Gly Asp Ala Trp Leu Asn Arg Thr Thr Arg
 85 90 95

Ser Ile Xaa Lys Pro Lys Phe Ala Thr Gly Asn Gly Ala Thr Asp Trp
 100 105 110

Arg Pro Ala Gly Phe Leu Gln Ala His Asn Leu Lys Gly Gly Tyr Asn
 115 120 125

His Ala Tyr Asp Arg Gly His Leu Leu Ala Tyr Ala Leu Val Gly Gly

130	135	140
Ile His Gly Phe Asp Ala Ser Glu Ser Asn Pro Ser Asn Ile Ala Thr		
145	150	155 160
Gln Thr Ala Trp Ala Asn Glu Ala Arg Ser Lys Asn Ser Thr Gly Gln		
	165	170 175
Asn Tyr Tyr Glu Gly Leu Val Arg Lys Ala Leu Asp Gln Asn Lys Gln		
	180	185 190
Val Arg Tyr Arg Val Thr Asn Ile Tyr Asp Gly Asn Asn Ile Val Pro		
	195	200 205
Ala Gly Ala His Ile Glu Ala Lys Ser Ser Asp Gly Ser Leu Glu Tyr		
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Thr Gly		

<210> 23
 <211> 18
 <212> DNA
 <213> Lactobacillus reuteri

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18

<210> 24
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 <212> DNA
 <213> Lactobacillus reuteri

<400> 24
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18

<210> 25
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 <212> DNA
 <213> Lactobacillus reuteri

<400> 25

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<211> 7113

<212> DNA

<213> *Lactobacillus reuteri*

<220>

<221> unsure

<222> (3109)

<220>

<221> unsure

<222> (3394)

<400> 26

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<222> (3)..(941)

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gca atg att att ctt ggt tta ctg gtt atc gtt ctt ggg tta ggt aat 95
  Ala Met Ile Ile Leu Gly Leu Leu Val Ile Val Leu Gly Leu Gly Asn
             20             25             30

aac tgg cac cca gtt ggg att tct aat ttg tgg tct cat ggc gga ttc 143
  Asn Trp His Pro Val Gly Ile Ser Asn Leu Trp Ser His Gly Gly Phe
             35             40             45

ttt acc ggt ggc ttt atg ggc ttt atg ttc tcg cta tct gtg att gct 191
  Phe Thr Gly Gly Phe Met Gly Phe Met Phe Ser Leu Ser Val Ile Ala
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ggt tct tat cag gga att gag tta ttg gga atc act gct ggt gaa gct 239
  Gly Ser Tyr Gln Gly Ile Glu Leu Leu Gly Ile Thr Ala Gly Glu Ala
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gaa tca cca cgt cat gcg att gtg aaa tca gtt aag tcc gtt atc tgg 287
  Glu Ser Pro Arg His Ala Ile Val Lys Ser Val Lys Ser Val Ile Trp
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cgg atc tta atc ttc tat att ggt gca att ttc gtc att gtt tct att 335
  Arg Ile Leu Ile Phe Tyr Ile Gly Ala Ile Phe Val Ile Val Ser Ile
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tac cca tgg aac gaa ttg aag tcc gtt ggc tca cca ttc gtt gaa acc 383
  Tyr Pro Trp Asn Glu Leu Lys Ser Val Gly Ser Pro Phe Val Glu Thr

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gtt ttg acg gca gct ctt tct gga gct aac tct gga att tac agt gct			479
Val Leu Thr Ala Ala Leu Ser Gly Ala Asn Ser Gly Ile Tyr Ser Ala			
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agt cgg atg ttg ttc aag ctt tct gtt gat ggg gaa gta cca aag ttc			527
Ser Arg Met Leu Phe Lys Leu Ser Val Asp Gly Glu Val Pro Lys Phe			
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Ile Phe Ser Ser Ala Ala Gln Asn Ile Phe Val Ile Val Tyr Ser Ser			
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agt gtt ctt cca ggg atg gta cca tgg ttt atc att ctc ttg tca gaa			719
Ser Val Leu Pro Gly Met Val Pro Trp Phe Ile Ile Leu Leu Ser Glu			
225	230	235	
ctt cac ttc aga aaa gaa cac cct gaa cag ctt aaa gat cat cca ttc			767
Leu His Phe Arg Lys Glu His Pro Glu Gln Leu Lys Asp His Pro Phe			
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aag atg ccg ctt tac ccg gct tat aac tac ttt agt ttg att gcc ttg			815
Lys Met Pro Leu Tyr Pro Ala Tyr Asn Tyr Phe Ser Leu Ile Ala Leu			
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act gtg atc ttg atc ttc atg ttc ttt aac cca gat act cga gtt tca			863
Thr Val Ile Leu Ile Phe Met Phe Phe Asn Pro Asp Thr Arg Val Ser			
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gta tca gtt ggt gtt atc ttc ttg att atc atg agt att att tat cgt			911
Val Ser Val Gly Val Ile Phe Leu Ile Ile Met Ser Ile Ile Tyr Arg			
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<212> PRT

<213> *Lactobacillus reuteri*

<400> 28

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 Trp His Pro Val Gly Ile Ser Asn Leu Trp Ser His Gly Gly Phe Phe
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 Thr Gly Gly Phe Met Gly Phe Met Phe Ser Leu Ser Val Ile Ala Gly
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 Ser Tyr Gln Gly Ile Glu Leu Leu Gly Ile Thr Ala Gly Glu Ala Glu
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 Ser Pro Arg His Ala Ile Val Lys Ser Val Lys Ser Val Ile Trp Arg
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 Ile Leu Ile Phe Tyr Ile Gly Ala Ile Phe Val Ile Val Ser Ile Tyr
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310

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<211> 600

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<213> Lactobacillus reuteri

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<222> (1)..(597)

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Ile Arg Pro Lys His Asn Gln Lys Tyr Ser Leu Glu Thr Lys Leu Thr
           20           25           30

gct gta aaa gct tat ctt tct ggc aag tat act aat caa gca att ctc      144
Ala Val Lys Ala Tyr Leu Ser Gly Lys Tyr Thr Asn Gln Ala Ile Leu
           35           40           45

cag cag tat caa att aga aat att tct caa cta cat caa tgg gtt atc      192
Gln Gln Tyr Gln Ile Arg Asn Ile Ser Gln Leu His Gln Trp Val Ile
           50           55           60

agt tac aat aat gac aaa ctc cga gtt aat cag aca acg aga aag cga      240
Ser Tyr Asn Asn Asp Lys Leu Arg Val Asn Gln Thr Thr Arg Lys Arg
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gtc aga aaa atg gga cga aaa gta acc ttt gat gaa aag agg cag att      288
Val Arg Lys Met Gly Arg Lys Val Thr Phe Asp Glu Lys Arg Gln Ile
           85           90           95

gtc cga tgg aca att gaa cat aac aat aac tat aaa gcg gct gca gag      336
Val Arg Trp Thr Ile Glu His Asn Asn Asn Tyr Lys Ala Ala Ala Glu
           100           105           110

aag tat gat att agt tac caa cga gtt tat tct tgg gta cgg aag tac      384
Lys Tyr Asp Ile Ser Tyr Gln Arg Val Tyr Ser Trp Val Arg Lys Tyr
           115           120           125

cga gta aat agc gac tgg gaa gta cta aaa gat aac cgt ggg cgt aat      432
Arg Val Asn Ser Asp Trp Glu Val Leu Lys Asp Asn Arg Gly Arg Asn

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130

135

140

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 Arg Glu Leu Glu Asp Arg Asp Arg Glu Arg Glu Leu Gln Ile Ala Phe
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gca aaa aaa tta gtc gaa ata cgc aat cgg gag gtg aaa cga ccg gac 576
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<213> Lactobacillus reuteri

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Ala Val Lys Ala Tyr Leu Ser Gly Lys Tyr Thr Asn Gln Ala Ile Leu
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Gln Gln Tyr Gln Ile Arg Asn Ile Ser Gln Leu His Gln Trp Val Ile
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Ser Tyr Asn Asn Asp Lys Leu Arg Val Asn Gln Thr Thr Arg Lys Arg
 65 70 75 80

Val Arg Lys Met Gly Arg Lys Val Thr Phe Asp Glu Lys Arg Gln Ile
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Val Arg Trp Thr Ile Glu His Asn Asn Asn Tyr Lys Ala Ala Ala Glu
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Lys Tyr Asp Ile Ser Tyr Gln Arg Val Tyr Ser Trp Val Arg Lys Tyr
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Arg Val Asn Ser Asp Trp Glu Val Leu Lys Asp Asn Arg Gly Arg Asn
 130 135 140

Lys Gly Lys Glu Pro Thr Asn Glu Leu Glu Lys Leu Arg Lys Arg Val
 145 150 155 160

Arg Glu Leu Glu Asp Arg Asp Arg Glu Arg Glu Leu Gln Ile Ala Phe
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<212> DNA

<213> Lactobacillus reuteri

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 Ile Thr Arg Gln Ala Tyr Tyr Lys Trp Leu Lys His Glu Pro Thr Lys
 20 25 30

tat gag att gaa gaa tcg gag att ctc caa ttg att aaa cag tta gaa 144
 Tyr Glu Ile Glu Glu Ser Glu Ile Leu Gln Leu Ile Lys Gln Leu Glu
 35 40 45

aat gaa cat aag caa agc gtt ggt tat gac aaa atg act agg tta atc 192
 Asn Glu His Lys Gln Ser Val Gly Tyr Asp Lys Met Thr Arg Leu Ile
 50 55 60

aag tta agt cag cag atc tct tat acc gtt aat aag aaa cga gtc att 240
 Lys Leu Ser Gln Gln Ile Ser Tyr Thr Val Asn Lys Lys Arg Val Ile
 65 70 75 80

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Arg Ile Met Lys Gly His Ser Ile Lys Ala Asp Tyr Arg Gln Pro Thr	
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Asp Lys Arg Ile Gln Ala Gln Gln Thr Tyr Glu Ala Glu Asn Ile Leu	
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Ile Val Leu Asp Leu Tyr Gly Gln Tyr Pro Val Ser Trp Leu Ile Thr	
145 150 155 160	
 cct aca gaa acc gct gaa gga gta gtt caa gtg ttc gag caa gca cgg	528
Pro Thr Glu Thr Ala Glu Gly Val Val Gln Val Phe Glu Gln Ala Arg	
165 170 175	
 atg aaa gaa gga gca cta gct ccg tta att cat act gat cgt ggt gcg	576
Met Lys Glu Gly Ala Leu Ala Pro Leu Ile His Thr Asp Arg Gly Ala	
180 185 190	
 gcg tat act tcc aaa gca ttt aat cag tat tta gta gtt aat ggt gcc	624
Ala Tyr Thr Ser Lys Ala Phe Asn Gln Tyr Leu Val Val Asn Gly Ala	
195 200 205	
 caa cac agt tat tca gca cca ggg aca ccg gct gac aat gcc gta ata	672
Gln His Ser Tyr Ser Ala Pro Gly Thr Pro Ala Asp Asn Ala Val Ile	
210 215 220	
 gaa cat tgg tgg gca gat ttt aag gct att tgg atc gca cat cta cct	720
Glu His Trp Trp Ala Asp Phe Lys Ala Ile Trp Ile Ala His Leu Pro	
225 230 235 240	
 aaa gca caa aca tta tta gaa cta gaa gaa caa gtt aga gaa gga att	768
Lys Ala Gln Thr Leu Leu Glu Leu Glu Glu Gln Val Arg Glu Gly Ile	
245 250 255	
 acc tat ttc act gaa aaa ttt atc tca gcg aag aga aat gac ctt acc	816
Thr Tyr Phe Thr Glu Lys Phe Ile Ser Ala Lys Arg Asn Asp Leu Thr	
260 265 270	

gca gcg gaa tac cgc ttt ggc aag gcc aac taa
 Ala Ala Glu Tyr Arg Phe Gly Lys Ala Asn
 275 280

849

<210> 32

<211> 282

<212> PRT

<213> *Lactobacillus reuteri*

<400> 32

Met Asn Asn Glu Gly Tyr Ser Ile Ser Glu Leu Ala Lys Val Ala Gly
 1 5 10 15
 Ile Thr Arg Gln Ala Tyr Tyr Lys Trp Leu Lys His Glu Pro Thr Lys
 20 25 30
 Tyr Glu Ile Glu Glu Ser Glu Ile Leu Gln Leu Ile Lys Gln Leu Glu
 35 40 45
 Asn Glu His Lys Gln Ser Val Gly Tyr Asp Lys Met Thr Arg Leu Ile
 50 55 60
 Lys Leu Ser Gln Gln Ile Ser Tyr Thr Val Asn Lys Lys Arg Val Ile
 65 70 75 80
 Arg Ile Met Lys Gly His Ser Ile Lys Ala Asp Tyr Arg Gln Pro Thr
 85 90 95
 Asp Lys Arg Ile Gln Ala Gln Gln Thr Tyr Glu Ala Glu Asn Ile Leu
 100 105 110
 Asn Arg Gln Phe Asp Gln Thr Ala Ala Asn Gln Val Trp Val Thr Asp
 115 120 125
 Thr Thr Glu Leu Asn Tyr Gly Ile Trp Leu Asn Lys Val Arg Leu His
 130 135 140
 Ile Val Leu Asp Leu Tyr Gly Gln Tyr Pro Val Ser Trp Leu Ile Thr
 145 150 155 160
 Pro Thr Glu Thr Ala Glu Gly Val Val Gln Val Phe Glu Gln Ala Arg
 165 170 175
 Met Lys Glu Gly Ala Leu Ala Pro Leu Ile His Thr Asp Arg Gly Ala
 180 185 190
 Ala Tyr Thr Ser Lys Ala Phe Asn Gln Tyr Leu Val Val Asn Gly Ala
 195 200 205
 Gln His Ser Tyr Ser Ala Pro Gly Thr Pro Ala Asp Asn Ala Val Ile
 210 215 220
 Glu His Trp Trp Ala Asp Phe Lys Ala Ile Trp Ile Ala His Leu Pro
 225 230 235 240
 Lys Ala Gln Thr Leu Leu Glu Leu Glu Glu Gln Val Arg Glu Gly Ile
 245 250 255
 Thr Tyr Phe Thr Glu Lys Phe Ile Ser Ala Lys Arg Asn Asp Leu Thr
 260 265 270
 Ala Ala Glu Tyr Arg Phe Gly Lys Ala Asn
 275 280

<210> 33
 <211> 744
 <212> DNA
 <213> Lactobacillus reuteri

<220>
 <221> CDS
 <222> (1)..(744)

<220>
 <221> unsure
 <222> (12)

<220>
 <221> unsure
 <222> (297)

<220>
 <221> misc_feature
 <222> (10)..(12)
 <223> Xaa = Tyr or stop

<220>
 <221> misc_feature
 <222> (295)..(297)
 <223> Xaa = Tyr or stop

<400> 33
 atg ctt cgt tan acc ata tta gta aaa ttg ctt att gga aga aaa cca 48
 Met Leu Arg Xaa Thr Ile Leu Val Lys Leu Leu Ile Gly Arg Lys Pro
 1 5 10 15
 gtc aca acg atc aaa aaa aca tta ccg cca act cag gaa cag gct aat 96
 Val Thr Thr Ile Lys Lys Thr Leu Pro Pro Thr Gln Glu Gln Ala Asn
 20 25 30
 tca gtc tta act ccg gct gtt cgc caa caa ctt ggc att tca att acc 144
 Ser Val Leu Thr Pro Ala Val Arg Gln Gln Leu Gly Ile Ser Ile Thr
 35 40 45
 tgg aac aaa gcc ggt gcg ttt att atc aat aat aac caa aca aat ctt 192
 Trp Asn Lys Ala Gly Ala Phe Ile Ile Asn Asn Asn Gln Thr Asn Leu
 50 55 60
 aac gct aag att gca agt gca ccc tat gct gta aat cat ctt gac cgt 240
 Asn Ala Lys Ile Ala Ser Ala Pro Tyr Ala Val Asn His Leu Asp Arg

65	70	75	80	
caa gga agg gcg tgg caa ggt gat gcc tgg tta aac agg aca act cgg				288
Gln Gly Arg Ala Trp Gln Gly Asp Ala Trp Leu Asn Arg Thr Thr Arg				
85		90	95	
tca ata tan aag ccg aaa ttt gcc aca ggg aat ggt gct acg gat tgg				336
Ser Ile Xaa Lys Pro Lys Phe Ala Thr Gly Asn Gly Ala Thr Asp Trp				
100	105		110	
cga cca gct ggc ttc ctt cag gcg cat aat ctt aaa ggc ggg tac aat				384
Arg Pro Ala Gly Phe Leu Gln Ala His Asn Leu Lys Gly Gly Tyr Asn				
115	120		125	
cat gca tac gat cgc gga cac ctt ctt gcc tat gca cta gtt ggt ggt				432
His Ala Tyr Asp Arg Gly His Leu Leu Ala Tyr Ala Leu Val Gly Gly				
130	135		140	
att cat gga ttt gat gca tcc gaa tca aat cca tct aat att gcc acg				480
Ile His Gly Phe Asp Ala Ser Glu Ser Asn Pro Ser Asn Ile Ala Thr				
145	150	155	160	
caa act gcc tgg gca aat gaa gca cga agt aag aac tca aca ggg caa				528
Gln Thr Ala Trp Ala Asn Glu Ala Arg Ser Lys Asn Ser Thr Gly Gln				
165	170		175	
aat tac tac gaa ggt ctg gtg aga aaa gca tta gat cag aat aag caa				576
Asn Tyr Tyr Glu Gly Leu Val Arg Lys Ala Leu Asp Gln Asn Lys Gln				
180	185		190	
gtt cgc tac cga gtt acc aat att tat gac ggt aat aat atc gtt ccg				624
Val Arg Tyr Arg Val Thr Asn Ile Tyr Asp Gly Asn Asn Ile Val Pro				
195	200		205	
gca ggt gct cat atc gaa gct aaa tct agt gat ggt tct cta gaa tac				672
Ala Gly Ala His Ile Glu Ala Lys Ser Ser Asp Gly Ser Leu Glu Tyr				
210	215		220	
aat gtc ttt gtt ccg aat gtc caa aga aac att acc att aat tat tca				720
Asn Val Phe Val Pro Asn Val Gln Arg Asn Ile Thr Ile Asn Tyr Ser				
225	230	235	240	
acc ggt gca gta aaa caa aac taa				744
Thr Gly Ala Val Lys Gln Asn				
245				

<210> 34

<211> 247

<212> PRT

<213> *Lactobacillus reuteri*

<400> 34

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Met Leu Arg Xaa Thr Ile Leu Val Lys Leu Leu Ile Gly Arg Lys Pro
 1              5              10              15
Val Thr Thr Ile Lys Lys Thr Leu Pro Pro Thr Gln Glu Gln Ala Asn
      20              25              30
Ser Val Leu Thr Pro Ala Val Arg Gln Gln Leu Gly Ile Ser Ile Thr
      35              40              45
Trp Asn Lys Ala Gly Ala Phe Ile Ile Asn Asn Asn Gln Thr Asn Leu
      50              55              60
Asn Ala Lys Ile Ala Ser Ala Pro Tyr Ala Val Asn His Leu Asp Arg
      65              70              75              80
Gln Gly Arg Ala Trp Gln Gly Asp Ala Trp Leu Asn Arg Thr Thr Arg
      85              90              95
Ser Ile Xaa Lys Pro Lys Phe Ala Thr Gly Asn Gly Ala Thr Asp Trp
      100              105              110
Arg Pro Ala Gly Phe Leu Gln Ala His Asn Leu Lys Gly Gly Tyr Asn
      115              120              125
His Ala Tyr Asp Arg Gly His Leu Leu Ala Tyr Ala Leu Val Gly Gly
      130              135              140
Ile His Gly Phe Asp Ala Ser Glu Ser Asn Pro Ser Asn Ile Ala Thr
      145              150              155              160
Gln Thr Ala Trp Ala Asn Glu Ala Arg Ser Lys Asn Ser Thr Gly Gln
      165              170              175
Asn Tyr Tyr Glu Gly Leu Val Arg Lys Ala Leu Asp Gln Asn Lys Gln
      180              185              190
Val Arg Tyr Arg Val Thr Asn Ile Tyr Asp Gly Asn Asn Ile Val Pro
      195              200              205
Ala Gly Ala His Ile Glu Ala Lys Ser Ser Asp Gly Ser Leu Glu Tyr
      210              215              220
Asn Val Phe Val Pro Asn Val Gln Arg Asn Ile Thr Ile Asn Tyr Ser
      225              230              235              240
Thr Gly Ala Val Lys Gln Asn
      245

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<210> 35

<211> 1540

<212> DNA

<213> *Lactobacillus reuteri*

<220>

<221> CDS

<222> (1)..(1539)

<400> 35

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  1           5           10           15

gat ggt caa gaa aca cca cca tta aag atc cat caa tta ttt gat tca      96
Asp Gly Gln Glu Thr Pro Pro Leu Lys Ile His Gln Leu Phe Asp Ser
          20           25           30

caa aaa tac gat cag tta atc gca gta act ggg aaa att act gct gac      144
Gln Lys Tyr Asp Gln Leu Ile Ala Val Thr Gly Lys Ile Thr Ala Asp
          35           40           45

ttc att aat aaa tac ctt agt aat ttt atc agt att aat gta gcg tta      192
Phe Ile Asn Lys Tyr Leu Ser Asn Phe Ile Ser Ile Asn Val Ala Leu
          50           55           60

agc tcc caa tca act agt gaa tta agt gct gat gag atg gtg aca aag      240
Ser Ser Gln Ser Thr Ser Glu Leu Ser Ala Asp Glu Met Val Thr Lys
          65           70           75           80

gtt gca ctt acc aat gct ctc ctt agt tca gca aat aaa gaa gct gct      288
Val Ala Leu Thr Asn Ala Leu Leu Ser Ser Ala Asn Lys Glu Ala Ala
          85           90           95

aaa ctc ttc tca gcg tta acc agt gac aac caa acg aac gtc tta aat      336
Lys Leu Phe Ser Ala Leu Thr Ser Asp Asn Gln Thr Asn Val Leu Asn
          100           105           110

aat ctt ttt cgc gta tca atc gcg cct act cag gtt atc cat tct aag      384
Asn Leu Phe Arg Val Ser Ile Ala Pro Thr Gln Val Ile His Ser Lys
          115           120           125

ttt tac ttg tta agt agt tca act act cat gat tcc cgt gtg att ctt      432
Phe Tyr Leu Leu Ser Ser Ser Thr Thr His Asp Ser Arg Val Ile Leu
          130           135           140

ggg agt gta gat tta gac gaa gct tca ttt gat gct cac cga aat caa      480
Gly Ser Val Asp Leu Asp Glu Ala Ser Phe Asp Ala His Arg Asn Gln
          145           150           155           160

ttt gaa gaa gta ttg gta ttt gac aat gat gtc cgc tta tac caa aac      528
Phe Glu Glu Val Leu Val Phe Asp Asn Asp Val Arg Leu Tyr Gln Asn
          165           170           175

ctt act gac cac ttt aaa aag gat ttt aag cca gta ttg aag ccc ttc      576
Leu Thr Asp His Phe Lys Lys Asp Phe Lys Pro Val Leu Lys Pro Phe

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180	185	190	
ttt act atg aac cta gta aag gca gct caa aag caa gtt gag gaa gga			624
Phe Thr Met Asn Leu Val Lys Ala Ala Gln Lys Gln Val Glu Glu Gly			
195	200	205	
aag aaa gat cag gat agc ggt aag gga ccg gtt atc ctt gat aat gaa			672
Lys Lys Asp Gln Asp Ser Gly Lys Gly Pro Val Ile Leu Asp Asn Glu			
210	215	220	
aca aca gat aag atc gct gaa aca gac atg gtg gat ctg ttg aag cat			720
Thr Thr Asp Lys Ile Ala Glu Thr Asp Met Val Asp Leu Leu Lys His			
225	230	235	240
gac ctt cag cat gat att gac cat aat ctt gtt cct gaa atg atc aca			768
Asp Leu Gln His Asp Ile Asp His Asn Leu Val Pro Glu Met Ile Thr			
245	250	255	
aag tca atg cgt gat att acc ata aat cgt tct caa gca aag gag aaa			816
Lys Ser Met Arg Asp Ile Thr Ile Asn Arg Ser Gln Ala Lys Glu Lys			
260	265	270	
att gct aag cag gtt aag caa cat gat acg att tat act ttg caa aaa			864
Ile Ala Lys Gln Val Lys Gln His Asp Thr Ile Tyr Thr Leu Gln Lys			
275	280	285	
gaa gcg gtc tct cct cgg gca gct aag cca aaa cta aag act cga gaa			912
Glu Ala Val Ser Pro Arg Ala Ala Lys Pro Lys Leu Lys Thr Arg Glu			
290	295	300	
aaa att acc aag cag gtt cag gat gct ttg atc agt gga atg tca cca			960
Lys Ile Thr Lys Gln Val Gln Asp Ala Leu Ile Ser Gly Met Ser Pro			
305	310	315	320
cag caa cgg gat gct gag aaa aag tac acg act ttt ctg tac gat cgg			1008
Gln Gln Arg Asp Ala Glu Lys Lys Tyr Thr Thr Phe Leu Tyr Asp Arg			
325	330	335	
cca atg gaa cga aac att gcg aat aac aat agt ggc cta tac gtt cct			1056
Pro Met Glu Arg Asn Ile Ala Asn Asn Asn Ser Gly Leu Tyr Val Pro			
340	345	350	
aat gat acg gga act cac cca atc cca ttt ggt aaa att gca act att			1104
Asn Asp Thr Gly Thr His Pro Ile Pro Phe Gly Lys Ile Ala Thr Ile			
355	360	365	
tct gaa att cgt gac ggt tta aag agc att gat gct gtt atg aag ggc			1152
Ser Glu Ile Arg Asp Gly Leu Lys Ser Ile Asp Ala Val Met Lys Gly			

370	375	380	
tat cag cag ttt gtc gtt gat tat gat gct gac tac ggg aag cgg ttc			1200
Tyr Gln Gln Phe Val Val Asp Tyr Asp Ala Asp Tyr Gly Lys Arg Phe			
385	390	395	400
ttt gaa gca att ttg tat agt ttt act gca ccg ttt tta tgg gaa att			1248
Phe Glu Ala Ile Leu Tyr Ser Phe Thr Ala Pro Phe Leu Trp Glu Ile			
405	410		415
cgt tct aaa gct agc ctg aac cct gaa gat ggg aat gat gtt cct aat			1296
Arg Ser Lys Ala Ser Leu Asn Pro Glu Asp Gly Asn Asp Val Pro Asn			
420	425		430
ttc cta atc cta ggg gca acg gct ggt tcc gga aag tct acc ctt ctt			1344
Phe Leu Ile Leu Gly Ala Thr Ala Gly Ser Gly Lys Ser Thr Leu Leu			
435	440		445
cgg att att aat cag ctc acg tgg aac act gat cgc tcg ttg att gac			1392
Arg Ile Ile Asn Gln Leu Thr Trp Asn Thr Asp Arg Ser Leu Ile Asp			
450	455		460
ttt gga acg atc tac ccg tcg caa act cct caa aag aag gca aag act			1440
Phe Gly Thr Ile Tyr Pro Ser Gln Thr Pro Gln Lys Lys Ala Lys Thr			
465	470	475	480
gtt gag gcg atg gaa cat tat atg aaa ctt ggt agt tca tac ccg gtt			1488
Val Glu Ala Met Glu His Tyr Met Lys Leu Gly Ser Ser Tyr Pro Val			
485	490		495
ttg tta gat gaa att gaa ccg tac ttc ttc cag caa gat caa tat agt			1536
Leu Leu Asp Glu Ile Glu Pro Tyr Phe Phe Gln Gln Asp Gln Tyr Ser			
500	505		510
cga c			1540
Arg			

<210> 36

<211> 513

<212> PRT

<213> Lactobacillus reuteri

<400> 36

Met Val Met Thr Glu Thr Ala Gly Ile Arg Lys Ile His Ile Val Phe

1

5

10

15

Asp Gly Gln Glu Thr Pro Pro Leu Lys Ile His Gln Leu Phe Asp Ser

20	25	30
Gln Lys Tyr Asp Gln Leu Ile Ala Val Thr Gly Lys Ile Thr Ala Asp		
35	40	45
Phe Ile Asn Lys Tyr Leu Ser Asn Phe Ile Ser Ile Asn Val Ala Leu		
50	55	60
Ser Ser Gln Ser Thr Ser Glu Leu Ser Ala Asp Glu Met Val Thr Lys		
65	70	75
Val Ala Leu Thr Asn Ala Leu Leu Ser Ser Ala Asn Lys Glu Ala Ala		
85	90	95
Lys Leu Phe Ser Ala Leu Thr Ser Asp Asn Gln Thr Asn Val Leu Asn		
100	105	110
Asn Leu Phe Arg Val Ser Ile Ala Pro Thr Gln Val Ile His Ser Lys		
115	120	125
Phe Tyr Leu Leu Ser Ser Ser Thr Thr His Asp Ser Arg Val Ile Leu		
130	135	140
Gly Ser Val Asp Leu Asp Glu Ala Ser Phe Asp Ala His Arg Asn Gln		
145	150	155
Phe Glu Glu Val Leu Val Phe Asp Asn Asp Val Arg Leu Tyr Gln Asn		
165	170	175
Leu Thr Asp His Phe Lys Lys Asp Phe Lys Pro Val Leu Lys Pro Phe		
180	185	190
Phe Thr Met Asn Leu Val Lys Ala Ala Gln Lys Gln Val Glu Glu Gly		
195	200	205
Lys Lys Asp Gln Asp Ser Gly Lys Gly Pro Val Ile Leu Asp Asn Glu		
210	215	220
Thr Thr Asp Lys Ile Ala Glu Thr Asp Met Val Asp Leu Leu Lys His		
225	230	235
Asp Leu Gln His Asp Ile Asp His Asn Leu Val Pro Glu Met Ile Thr		
245	250	255
Lys Ser Met Arg Asp Ile Thr Ile Asn Arg Ser Gln Ala Lys Glu Lys		
260	265	270
Ile Ala Lys Gln Val Lys Gln His Asp Thr Ile Tyr Thr Leu Gln Lys		

275	280	285
Glu Ala Val Ser Pro Arg Ala Ala Lys Pro Lys Leu Lys Thr Arg Glu		
290	295	300
Lys Ile Thr Lys Gln Val Gln Asp Ala Leu Ile Ser Gly Met Ser Pro		
305	310	315
Gln Gln Arg Asp Ala Glu Lys Lys Tyr Thr Thr Phe Leu Tyr Asp Arg		
325	330	335
Pro Met Glu Arg Asn Ile Ala Asn Asn Asn Ser Gly Leu Tyr Val Pro		
340	345	350
Asn Asp Thr Gly Thr His Pro Ile Pro Phe Gly Lys Ile Ala Thr Ile		
355	360	365
Ser Glu Ile Arg Asp Gly Leu Lys Ser Ile Asp Ala Val Met Lys Gly		
370	375	380
Tyr Gln Gln Phe Val Val Asp Tyr Asp Ala Asp Tyr Gly Lys Arg Phe		
385	390	395
Phe Glu Ala Ile Leu Tyr Ser Phe Thr Ala Pro Phe Leu Trp Glu Ile		
405	410	415
Arg Ser Lys Ala Ser Leu Asn Pro Glu Asp Gly Asn Asp Val Pro Asn		
420	425	430
Phe Leu Ile Leu Gly Ala Thr Ala Gly Ser Gly Lys Ser Thr Leu Leu		
435	440	445
Arg Ile Ile Asn Gln Leu Thr Trp Asn Thr Asp Arg Ser Leu Ile Asp		
450	455	460
Phe Gly Thr Ile Tyr Pro Ser Gln Thr Pro Gln Lys Lys Ala Lys Thr		
465	470	475
Val Glu Ala Met Glu His Tyr Met Lys Leu Gly Ser Ser Tyr Pro Val		
485	490	495
Leu Leu Asp Glu Ile Glu Pro Tyr Phe Phe Gln Gln Asp Gln Tyr Ser		
500	505	510
Arg		

<210> 37
<211> 26
<212> DNA
<213> Lactobacillus reuteri

<220>
<221> terminator
<222> (1)..(26)

<400> 37
aaagaagctg aaatttcggc ttcttt

26

<210> 38
<211> 28
<212> DNA
<213> Lactobacillus reuteri

<400> 38
gcagtcgacg gagttaagac tgaattag

28

<210> 39
<211> 26
<212> DNA
<213> Lactobacillus reuteri

<400> 39
ctagtcgacg cagtttctgt catgac

26

<210> 40
<211> 32
<212> DNA
<213> Lactobacillus reuteri

<400> 40
catatgtatt attcaaacgg gaattatgaa gc

32

<210> 41
<211> 30
<212> DNA
<213> Lactobacillus reuteri

<400> 41
tgatcatcta taccagcagt ttctgtcatg

30

<210> 42

<211> 35

<212> PRT

<213> Propionibacterium acnes

<400> 42

Ser Ile Ser Lys Asp Ser Arg Ile Ala Ile Ile Gly Ala Gly Pro Ala
1 5 10 15

Gly Leu Ala Ala Gly Met Tyr Leu Trp Gln Ala Gly Phe Xaa Asp Tyr
20 25 30

Thr Ile Leu
35

<210> 43

<211> 21

<212> PRT

<213> Clostridium sporogenes

<400> 43

Met Phe Asn Leu Lys Asn Arg Asn Phe Leu Thr Leu Met Asp Phe Thr
1 5 10 15

Pro Xaa Glu Ile Gln
20

<210> 44

<211> 14

<212> PRT

<213> Propionibacterium acnes

<400> 44

Lys Tyr Leu Asp Phe Val Thr Met Met Ser Phe Ala Lys Gly
1 5 10

<210> 45

<211> 9

<212> PRT

<213> Propionibacterium acnes

<400> 45

Lys Asp Leu Val Thr Arg Phe Phe Val

1

5

<210> 46
<211> 15
<212> PRT
<213> Propionibacterium acnes

<220>
<221> UNSURE
<222> (2)
<223> Xaa = Ile or Ser

<220>
<221> UNSURE
<222> (4)
<223> Xaa = His or Phe

<220>
<221> UNSURE
<222> (6)
<223> Xaa = Glu or Gln

<220>
<221> UNSURE
<222> (10)
<223> Xaa = Asp or Thr

<220>
<221> UNSURE
<222> (12)
<223> Xaa = Gly or Ser

<400> 46
Lys Xaa Ile Xaa Gln Xaa Tyr Met Val Xaa Ala Xaa Leu Val Lys
1 5 10 15

<210> 47
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 47
atcgcgatna tnggngcngg

20

<210> 48

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 48

ccngcytgcc anarrtacat

20

<210> 49

<211> 62

<212> DNA

<213> Propionibacterium acnes

<400> 49

atcgagatva trggggctgg cccggccggg ctggctgccg gaatgtacct ctggcargcs 60
gg 62

<210> 50

<211> 21

<212> PRT

<213> Propionibacterium acnes

<220>

<221> UNSURE

<222> (2)

<223> xaa = ala or glu

<220>

<221> UNSURE

<222> (3)..(4)

<223> xaa = ile or met

<400> 50

Ile Xaa Xaa Xaa Gly Ala Gly Pro Ala Gly Leu Ala Ala Gly Met Tyr
1 5 10 15

Leu Trp Gln Ala Gly
20

<210> 51

<211> 17
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 51

gggccagccc cyatnat

17

<210> 52
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 52

gctggctgcc ggaatgta

18

<210> 53
 <211> 569
 <212> DNA
 <213> Propionibacterium acnes

<400> 53

ggatcccaac tggccgcctg ccccggggga ggagtaccac gccgacatcg aaggcaacaa 60
 tgcccgtaac ggggtggaccg aggacacccc ggccgtcaat gatgcccagg ccgagcggcg 120
 ggccaaggag ctggcagcac atctcgatga gatggcacgt ggtcggcgaa ctgcccgtcg 180
 agatgtttcg cgacctatac cattaccgac ccatttcac gccgaactta ttcaccacta 240
 catcgacaag gaagaacgat gtccatctcg aaggattcac gtatcgccat catcggggct 300
 ggcccggccg ggctggctgc cggaatgtac ctcgaacagg ccggatttca cgactacacg 360
 atcctggaac gcaccgacca cgtcggaggc aagtgccact caccgaacta ccacggccgt 420
 cgttatgaga tggggggccat catgggcgtc cccagttacg acaccatcca ggagatcatg 480
 gatcgactg gcgacaaggt cgacggggccg aaactgcgtc gcgagttcct gcacgaggac 540
 ggcgagatct acgtcccgga aaaggatcc 569

<210> 54
 <211> 104
 <212> PRT
 <213> Propionibacterium acnes

<400> 54

Met Ser Ile Ser Lys Asp Ser Arg Ile Ala Ile Ile Gly Ala Gly Pro

1 5 10 15
Ala Gly Leu Ala Ala Gly Met Tyr Leu Glu Gln Ala Gly Phe His Asp
20 25 30
Tyr Thr Ile Leu Glu Arg Thr Asp His Val Gly Gly Lys Cys His Ser
35 40 45
Pro Asn Tyr His Gly Arg Arg Tyr Glu Met Gly Ala Ile Met Gly Val
50 55 60
Pro Ser Tyr Asp Thr Ile Gln Glu Ile Met Asp Arg Thr Gly Asp Lys
65 70 75 80
Val Asp Gly Pro Lys Leu Arg Arg Glu Phe Leu His Glu Asp Gly Glu
85 90 95
Ile Tyr Val Pro Glu Lys Asp Pro
100

<210> 55
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 55
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17

<210> 56
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 56
tcacgtatcg ccatcatc

18

<210> 57
<211> 17
<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 57

aatccggcct gttcgag

17

<210> 58

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 58

aggacggcga gatctac

17

<210> 59

<211> 5275

<212> DNA

<213> Propionibacterium acnes

<400> 59

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gtcaatgtcg acacgtcgtc aagaccggcg cacgaaccgg ccaccgctcc cggteggttc 4200
gtcgtcagag atgcctgtca cgaggacctg cctgaagccg cggctgttca ggccgtgtgc 4260
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gacctcatca gccaacagct cggaacgcc acgtggtaag ggcgataccg tgcgcacggc 5220
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<210> 60

<211> 1275

<212> DNA

<213> *Propionibacterium acnes*

<220>

<221> CDS

<222> (1)..(1275)

<400> 60

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atg tcc atc tcg aag gat tca cgt atc gcc atc atc ggg gct ggc ccg 48
Met Ser Ile Ser Lys Asp Ser Arg Ile Ala Ile Ile Gly Ala Gly Pro
1 5 10 15

```

```

gcc ggg ctg gct gcc gga atg tac ctc gaa cag gcc gga ttt cac gac 96
Ala Gly Leu Ala Ala Gly Met Tyr Leu Glu Gln Ala Gly Phe His Asp
20 25 30

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```

tac acg atc ctg gaa cgc acc gac cac gtc gga ggc aag tgc cac tca 144
Tyr Thr Ile Leu Glu Arg Thr Asp His Val Gly Gly Lys Cys His Ser
35 40 45

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ccg aac tac cac ggc cgt cgt tat gag atg ggg gcc atc atg ggc gtc 192
Pro Asn Tyr His Gly Arg Arg Tyr Glu Met Gly Ala Ile Met Gly Val
50 55 60

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ccc agt tac gac acc atc cag gag atc atg gat cgc act ggc gac aag 240

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51

Glu Lys Phe Leu Asp Tyr Ser Asp Ala Asp Asp Asp Glu Arg Glu Tyr	
260	265 270
ttc tcg aag atc atc cac cag cag tac atg gtg gat gcc tgc ctg gtg	864
Phe Ser Lys Ile Ile His Gln Gln Tyr Met Val Asp Ala Cys Leu Val	
275	280 285
aag gag tac ccg acc atc tcc ggg tac gtc ccc gac aac atg agg ccc	912
Lys Glu Tyr Pro Thr Ile Ser Gly Tyr Val Pro Asp Asn Met Arg Pro	
290	295 300
gaa cgt ctc ggg cac gtc atg gtt tac tac cac cgc tgg gct gat gat	960
Glu Arg Leu Gly His Val Met Val Tyr Tyr His Arg Trp Ala Asp Asp	
305	310 315 320
ccg cac cag atc atc acg acc tac ctg cta cgt aac cat ccg gac tac	1008
Pro His Gln Ile Ile Thr Thr Tyr Leu Leu Arg Asn His Pro Asp Tyr	
325	330 335
gcg gac aag act cag gag gag tgc cgc cag atg gtc ctc gac gac atg	1056
Ala Asp Lys Thr Gln Glu Glu Cys Arg Gln Met Val Leu Asp Asp Met	
340	345 350
gag acc ttc ggt cat ccg gtc gag aag atc atc gag gag cag acc tgg	1104
Glu Thr Phe Gly His Pro Val Glu Lys Ile Ile Glu Glu Gln Thr Trp	
355	360 365
tac tac ttc ccg cac gtt agc tcg gag gac tac aag gcc ggg tgg tac	1152
Tyr Tyr Phe Pro His Val Ser Ser Glu Asp Tyr Lys Ala Gly Trp Tyr	
370	375 380
gag aag gtc gag gga atg cag ggt cgt cgc aac acc ttc tac gcc gga	1200
Glu Lys Val Glu Gly Met Gln Gly Arg Arg Asn Thr Phe Tyr Ala Gly	
385	390 395 400
gaa att atg agt ttc ggt aat ttc gac gag gtg tgc cac tac tcg aag	1248
Glu Ile Met Ser Phe Gly Asn Phe Asp Glu Val Cys His Tyr Ser Lys	
405	410 415
gac ctg gtg acg cgg ttc ttc gtg tga	1275
Asp Leu Val Thr Arg Phe Phe Val	
420	425

<210> 61

<211> 424

<212> PRT

<213> Propionibacterium acnes

<400> 61

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Met Ser Ile Ser Lys Asp Ser Arg Ile Ala Ile Ile Gly Ala Gly Pro
 1           5           10           15
Ala Gly Leu Ala Ala Gly Met Tyr Leu Glu Gln Ala Gly Phe His Asp
 20           25           30
Tyr Thr Ile Leu Glu Arg Thr Asp His Val Gly Gly Lys Cys His Ser
 35           40           45
Pro Asn Tyr His Gly Arg Arg Tyr Glu Met Gly Ala Ile Met Gly Val
 50           55           60
Pro Ser Tyr Asp Thr Ile Gln Glu Ile Met Asp Arg Thr Gly Asp Lys
 65           70           75           80
Val Asp Gly Pro Lys Leu Arg Arg Glu Phe Leu His Glu Asp Gly Glu
 85           90           95
Ile Tyr Val Pro Glu Lys Asp Pro Val Arg Gly Pro Gln Val Met Ala
100           105           110
Ala Val Gln Lys Leu Gly Gln Leu Leu Ala Thr Lys Tyr Gln Gly Tyr
115           120           125
Asp Ala Asn Gly His Tyr Asn Lys Val His Glu Asp Leu Met Leu Pro
130           135           140
Phe Asp Glu Phe Leu Ala Leu Asn Gly Cys Glu Ala Ala Arg Asp Leu
145           150           155           160
Trp Ile Asn Pro Phe Thr Ala Phe Gly Tyr Gly His Phe Asp Asn Val
165           170           175
Pro Ala Ala Tyr Val Leu Lys Tyr Leu Asp Phe Val Thr Met Met Ser
180           185           190
Phe Ala Lys Gly Asp Leu Trp Thr Trp Ala Asp Gly Thr Gln Ala Met
195           200           205
Phe Glu His Leu Asn Ala Thr Leu Glu His Pro Ala Glu Arg Asn Val
210           215           220
Asp Ile Thr Arg Ile Thr Arg Glu Asp Gly Lys Val His Ile His Thr
225           230           235           240
Thr Asp Trp Asp Arg Glu Ser Asp Val Leu Val Leu Thr Val Pro Leu
245           250           255
Glu Lys Phe Leu Asp Tyr Ser Asp Ala Asp Asp Asp Glu Arg Glu Tyr
260           265           270
Phe Ser Lys Ile Ile His Gln Gln Tyr Met Val Asp Ala Cys Leu Val
275           280           285
Lys Glu Tyr Pro Thr Ile Ser Gly Tyr Val Pro Asp Asn Met Arg Pro
290           295           300
Glu Arg Leu Gly His Val Met Val Tyr Tyr His Arg Trp Ala Asp Asp
305           310           315           320
Pro His Gln Ile Ile Thr Thr Tyr Leu Leu Arg Asn His Pro Asp Tyr
325           330           335
Ala Asp Lys Thr Gln Glu Glu Cys Arg Gln Met Val Leu Asp Asp Met
340           345           350
Glu Thr Phe Gly His Pro Val Glu Lys Ile Ile Glu Glu Gln Thr Trp
355           360           365

```


Tyr Tyr Phe Pro His Val Ser Ser Glu Asp Tyr Lys Ala Gly Trp Tyr
 370 375 380
 Glu Lys Val Glu Gly Met Gln Gly Arg Arg Asn Thr Phe Tyr Ala Gly
 385 390 395 400
 Glu Ile Met Ser Phe Gly Asn Phe Asp Glu Val Cys His Tyr Ser Lys
 405 410 415
 Asp Leu Val Thr Arg Phe Phe Val
 420

<210> 62
 <211> 7
 <212> DNA
 <213> *Propionibacterium acnes*

<220>
 <221> RBS
 <222> (1) .. (7)

<400> 62
 aagggaag

7

<210> 63
 <211> 1073
 <212> DNA
 <213> *Propionibacterium acnes*

<400> 63
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 gcgcgataac ggtcggggaa ttgcttgggg gtgccaccga tatacatttt ggcggcattg 180
 cccgcgtca gtgtggtgac cgactcgacg gtaccgacat ccaccgttgg atagagggcg 240
 aggactgact tcggggcccc tattgagccg caggaactct tcaactttcc actggcggcg 300
 ccgtaggcga gattaatggc cattccacca ccagcggaat caccatgat cgatacctgt 360
 gaagggtcgc caccgagttc tttcacgtgg gacaggctcc agggccaggc acatgcgacc 420
 tgttttgggg cggtattcca ggtgggggtgg ccctgggtgg ccagggtgta cgagggggcga 480
 atgactaacc agccatgatc ggaaaaccat ctcaacgtgg cgggcatggt ggcgtcgggtg 540
 ctccatcctt caccatgaat gtcgacaagt accggggcat tgtggttatg ggcacggtag 600
 atctgggccc tctcgtcagg gccggatcca taccggaccg tttcgtcagg gtggtcggac 660
 atcgacgaca ccgcagctgc cgagacgacg ttgatacgtc caccggggcg gtccgtgatc 720
 caccgcgtcg tcgccgttgc cgccactggc acgatgaggg ccatcaccga gaagacaacg 780
 gccaccactc gcagaccacc tcgtcccaaa agagcgagga cgaaggcgat gacggcgatg 840
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 tgtgagggga ggatcgcggc cactgaccac gccagtaccg gcagggtcag gatcagcccg 960
 acgagaccgg aagtgatgcg tagccaggaa tgacgggagg ttttcgtgtc agccacgcgt 1020
 ccaccgtact cacgggacat ggtcgaatag atcttcgcgc aggaggggacc cat 1073

<210> 64

<211> 358

<212> PRT

<213> Propionibacterium acnes

<400> 64

Met Gly Pro Ser Cys Ala Lys Ile Leu Ser Thr Met Ser Arg Glu Tyr
1 5 10 15

Gly Gly Arg Val Ala Asp Thr Lys Thr Ser Arg His Ser Trp Leu Arg
20 25 30

Ile Thr Ser Gly Leu Val Gly Leu Ile Leu Thr Leu Pro Val Leu Ala
35 40 45

Trp Ser Val Ala Ala Ile Leu Pro Ser His Asn Ala Leu Thr Phe Ile
50 55 60

Ser Ser Val Leu Val Gly Ser Leu Ala Val Pro Ala Leu Val Ile Ala
65 70 75 80

Val Ile Ala Phe Val Leu Ala Leu Leu Gly Arg Gly Gly Leu Arg Val
85 90 95

Val Ala Val Val Phe Ser Val Met Ala Leu Ile Val Pro Val Ala Ala
100 105 110

Thr Ala Thr Thr Ala Trp Ile Thr Asp Arg Pro Gly Gly Arg Ile Asn
115 120 125

Val Val Ser Ala Ala Ala Val Ser Ser Met Ser Asp His Pro Asp Glu
130 135 140

Thr Val Arg Tyr Gly Ser Gly Pro Asp Glu Thr Ala Gln Ile Tyr Arg
145 150 155 160

Ala His Asn His Asn Ala Pro Val Leu Val Asp Ile His Gly Glu Gly
165 170 175

Trp Ser Thr Asp Ala Thr Met Pro Ala Thr Leu Arg Trp Phe Ser Asp
180 185 190

His Gly Trp Leu Val Ile Arg Pro Ser Tyr Thr Leu Ala Thr Gln Gly
195 200 205

His Pro Thr Trp Asn Thr Ala Pro Lys Gln Val Ala Cys Ala Trp Ala

210	215	220
Trp Ser Leu Ser His Val Lys Glu Leu Gly Gly Asp Pro Ser Gln Val		
225	230	235 240
Ser Ile Met Gly Asp Ser Ala Gly Gly Gly Met Ala Ile Asn Leu Ala		
245	250	255
Tyr Gly Ala Ala Ser Gly Lys Leu Lys Ser Ser Cys Gly Ser Ile Arg		
260	265	270
Ala Pro Lys Ser Val Leu Ala Leu Tyr Pro Thr Val Asp Val Gly Thr		
275	280	285
Val Glu Ser Val Thr Thr Leu Ser Ala Gly Asn Ala Ala Lys Met Tyr		
290	295	300
Ile Gly Gly Thr Pro Lys Gln Phe Pro Asp Arg Tyr Arg Ala Val Asn		
305	310	315 320
Ser Ser Thr Trp Ile Thr Pro Gln Ala Pro Pro Thr Met Val Ile Gln		
325	330	335
Gly Asn His Asp Thr Phe Val Pro Pro Ser Ser Val Arg Lys Phe Val		
340	345	350
Asn Arg Ala Arg Pro Ala		
355		

<210> 65
 <211> 783
 <212> DNA
 <213> Propionibacterium acnes

<220>
 <221> CDS
 <222> (1)..(783)

<400> 65	
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Met Ser Ile Thr Pro Arg Lys Cys Lys Ala Ala Ala Leu Ala Thr Ala	
1 5 10 15	
ccg gtg gcc gct gcc ctc ggt gct tac gga ttt ctt aaa ggg gcg acg	96
Pro Val Ala Ala Ala Leu Gly Ala Tyr Gly Phe Leu Lys Gly Ala Thr	
20 25 30	

aag ttc tat tcc agc cag gtt aac gga act ccc gag cag tac aag atg	144
Lys Phe Tyr Ser Ser Gln Val Asn Gly Thr Pro Glu Gln Tyr Lys Met	
35 40 45	
acc ctt cct ggt gac gac ctc gtc ccg gaa ggt tcg ccg cgc ttc aag	192
Thr Leu Pro Gly Asp Asp Leu Val Pro Glu Gly Ser Pro Arg Phe Lys	
50 55 60	
cgc ctc acc cat gtg gag gat ctc gac gcc ccc tgc gac gag gtc tgg	240
Arg Leu Thr His Val Glu Asp Leu Asp Ala Pro Cys Asp Glu Val Trp	
65 70 75 80	
aag cac gtc tac cag ctc aac acc acg acc gcc ggc ttc tac tcc ttc	288
Lys His Val Tyr Gln Leu Asn Thr Thr Thr Ala Gly Phe Tyr Ser Phe	
85 90 95	
acc ttc ttc gag aag atg ttc gga ctg tcg gtc gac aac acc ttc atg	336
Thr Phe Phe Glu Lys Met Phe Gly Leu Ser Val Asp Asn Thr Phe Met	
100 105 110	
gtg gaa cag gct tgg cag gcc ccg gac tac tac aag ccc ggt gac atg	384
Val Glu Gln Ala Trp Gln Ala Pro Asp Tyr Tyr Lys Pro Gly Asp Met	
115 120 125	
ttc tgt tgg agt tac gcc ggt ttc ggt gcc gag gtc gcc gac atg gtc	432
Phe Cys Trp Ser Tyr Ala Gly Phe Gly Ala Glu Val Ala Asp Met Val	
130 135 140	
ccc ggc aag tat ctg gtg tgg ttc gct gac acc cgt gac ggc acc agg	480
Pro Gly Lys Tyr Leu Val Trp Phe Ala Asp Thr Arg Asp Gly Thr Arg	
145 150 155 160	
aca ccg ggc gca agt ttc ctg cta ccg cct gga atg ccg tgg aac cgc	528
Thr Pro Gly Ala Ser Phe Leu Leu Pro Pro Gly Met Pro Trp Asn Arg	
165 170 175	
tgg agt tgg gtc atc gcc ctg gaa ccc ctc gac agt ggc aac cgg acg	576
Trp Ser Trp Val Ile Ala Leu Glu Pro Leu Asp Ser Gly Asn Arg Thr	
180 185 190	
cgc atc tac tcc cgg tgg aac atc tcg gcc tcc gag gag tcc agt ccg	624
Arg Ile Tyr Ser Arg Trp Asn Ile Ser Ala Ser Glu Glu Ser Ser Pro	
195 200 205	
atc tcg gtc ttc ctc atg gat ctg gtc atg atg gac ggc ggc ggc atg	672
Ile Ser Val Phe Leu Met Asp Leu Val Met Met Asp Gly Gly Gly Met	
210 215 220	

gtg aac cgt cgg atg ttc caa ggg ctg gag aag gct gcc gtc gga act 720
 Val Asn Arg Arg Met Phe Gln Gly Leu Glu Lys Ala Ala Val Gly Thr
 225 230 235 240

gct cgc aag aac atc gtt cct gcg cgc cta tca gcg gtt cat ggg caa 768
 Ala Arg Lys Asn Ile Val Pro Ala Arg Leu Ser Ala Val His Gly Gln
 245 250 255

gtc cta cgg cac tga 783
 Val Leu Arg His
 260

<210> 66

<211> 260

<212> PRT

<213> Propionibacterium acnes

<400> 66

Met Ser Ile Thr Pro Arg Lys Cys Lys Ala Ala Ala Leu Ala Thr Ala
 1 5 10 15
 Pro Val Ala Ala Ala Leu Gly Ala Tyr Gly Phe Leu Lys Gly Ala Thr
 20 25 30
 Lys Phe Tyr Ser Ser Gln Val Asn Gly Thr Pro Glu Gln Tyr Lys Met
 35 40 45
 Thr Leu Pro Gly Asp Asp Leu Val Pro Glu Gly Ser Pro Arg Phe Lys
 50 55 60
 Arg Leu Thr His Val Glu Asp Leu Asp Ala Pro Cys Asp Glu Val Trp
 65 70 75 80
 Lys His Val Tyr Gln Leu Asn Thr Thr Thr Ala Gly Phe Tyr Ser Phe
 85 90 95
 Thr Phe Phe Glu Lys Met Phe Gly Leu Ser Val Asp Asn Thr Phe Met
 100 105 110
 Val Glu Gln Ala Trp Gln Ala Pro Asp Tyr Tyr Lys Pro Gly Asp Met
 115 120 125
 Phe Cys Trp Ser Tyr Ala Gly Phe Gly Ala Glu Val Ala Asp Met Val
 130 135 140
 Pro Gly Lys Tyr Leu Val Trp Phe Ala Asp Thr Arg Asp Gly Thr Arg
 145 150 155 160
 Thr Pro Gly Ala Ser Phe Leu Leu Pro Pro Gly Met Pro Trp Asn Arg
 165 170 175
 Trp Ser Trp Val Ile Ala Leu Glu Pro Leu Asp Ser Gly Asn Arg Thr
 180 185 190
 Arg Ile Tyr Ser Arg Trp Asn Ile Ser Ala Ser Glu Glu Ser Ser Pro
 195 200 205
 Ile Ser Val Phe Leu Met Asp Leu Val Met Met Asp Gly Gly Gly Met
 210 215 220
 Val Asn Arg Arg Met Phe Gln Gly Leu Glu Lys Ala Ala Val Gly Thr

225	230	235	240
Ala Arg Lys Asn Ile Val Pro Ala Arg Leu Ser Ala Val His Gly Gln			
	245	250	255
Val Leu Arg His			
260			

<210> 67
 <211> 7
 <212> DNA
 <213> Propionibacterium acnes

<220>
 <221> RBS
 <222> (1) .. (7)

<400> 67
 gaaggag

7

<210> 68
 <211> 582
 <212> DNA
 <213> Propionibacterium acnes

<220>
 <221> CDS
 <222> (1) .. (582)

<400> 68

atg gat act tca gtc aat gtc gac acg tgc tca aga ccg gcg cac gaa	48
Met Asp Thr Ser Val Asn Val Asp Thr Ser Ser Arg Pro Ala His Glu	
1 5 10 15	
ccg gcc acc gct ccc ggt cgt ttc gtc gtc aga gat gcc tgt cac gag	96
Pro Ala Thr Ala Pro Gly Arg Phe Val Val Arg Asp Ala Cys His Glu	
20 25 30	
gac ctg cct gaa gcc gcg gct gtt cag gcc gtg tgc gtc cga gag atc	144
Asp Leu Pro Glu Ala Ala Ala Val Gln Ala Val Cys Val Arg Glu Ile	
35 40 45	
ggc cag ggg gtg atc cct aat gac gtc ctt acc gag gtc act ggc ccc	192
Gly Gln Gly Val Ile Pro Asn Asp Val Leu Thr Glu Val Thr Gly Pro	
50 55 60	
ggt atc gtc cac acc acc att gag cag tgg aac cac ttt atg gat gat	240

Gly Ile Val His Thr Thr Ile Glu Gln Trp Asn His Phe Met Asp Asp
 65 70 75 80
 ggt gcg atc ttc aag atc ctt gtt gat cgc ctc gat atg agg act gtc 288
 Gly Ala Ile Phe Lys Ile Leu Val Asp Arg Leu Asp Met Arg Thr Val
 85 90 95
 ggg gtt gcc atg gcc cgg gtc tct aca agt tct gat gct ccc aca ccg 336
 Gly Val Ala Met Ala Arg Val Ser Thr Ser Ser Asp Ala Pro Thr Pro
 100 105 110
 tgg gag atc gcg acc ctc cat gta ctg cca gag gcg cga aac tgc gga 384
 Trp Glu Ile Ala Thr Leu His Val Leu Pro Glu Ala Arg Asn Cys Gly
 115 120 125
 gcg tca gac aac ctc ctc gat gct tgt atc ggg aac cgg tcg gcc tat 432
 Ala Ser Asp Asn Leu Leu Asp Ala Cys Ile Gly Asn Arg Ser Ala Tyr
 130 135 140
 gtg tgg gtc ttt gcc gat aat gct cgc gcc att tcg ttc tac caa cgc 480
 Val Trp Val Phe Ala Asp Asn Ala Arg Ala Ile Ser Phe Tyr Gln Arg
 145 150 155 160
 cat ggg ttc cac gtc gac gcg gcc gac ggt gcc gtt gac gat tcc ctc 528
 His Gly Phe His Val Asp Ala Ala Asp Gly Ala Val Asp Asp Ser Leu
 165 170 175
 ggc ggg gta gag ctg cag cgg ctg atc cgc gag gac atc atc gag tcg 576
 Gly Gly Val Glu Leu Gln Arg Leu Ile Arg Glu Asp Ile Ile Glu Ser
 180 185 190
 cag tga 582
 Gln

<210> 69

<211> 193

<212> PRT

<213> Propionibacterium acnes

<400> 69

Met Asp Thr Ser Val Asn Val Asp Thr Ser Ser Arg Pro Ala His Glu
 1 5 10 15
 Pro Ala Thr Ala Pro Gly Arg Phe Val Val Arg Asp Ala Cys His Glu
 20 25 30
 Asp Leu Pro Glu Ala Ala Ala Val Gln Ala Val Cys Val Arg Glu Ile
 35 40 45
 Gly Gln Gly Val Ile Pro Asn Asp Val Leu Thr Glu Val Thr Gly Pro

50	55	60
Gly Ile Val His Thr Thr Ile Glu Gln Trp Asn His Phe Met Asp Asp		
65	70	75
Gly Ala Ile Phe Lys Ile Leu Val Asp Arg Leu Asp Met Arg Thr Val		80
	85	90
Gly Val Ala Met Ala Arg Val Ser Thr Ser Ser Asp Ala Pro Thr Pro		95
	100	105
Trp Glu Ile Ala Thr Leu His Val Leu Pro Glu Ala Arg Asn Cys Gly		110
	115	120
Ala Ser Asp Asn Leu Leu Asp Ala Cys Ile Gly Asn Arg Ser Ala Tyr		125
	130	135
Val Trp Val Phe Ala Asp Asn Ala Arg Ala Ile Ser Phe Tyr Gln Arg		140
	145	150
His Gly Phe His Val Asp Ala Ala Asp Gly Ala Val Asp Asp Ser Leu		155
	160	165
Gly Gly Val Glu Leu Gln Arg Leu Ile Arg Glu Asp Ile Ile Glu Ser		170
	175	180
	185	190
Gln		

<210> 70
 <211> 7
 <212> DNA
 <213> Propionibacterium acnes

<220>
 <221> RBS
 <222> (1)..(7)

<400> 70
 ggtagga

7

<210> 71
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<400> 71
 cagacatatg tccatctcga aggattc

27

<210> 72
 <211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 72

ctatctcgag tcacacgaag aaccgcgtc

29

<210> 73

<211> 53

<212> PRT

<213> Artificial Sequence

<220>

<221> UNSURE

<222> (2)

<220>

<221> UNSURE

<222> (4) .. (5)

<220>

<221> UNSURE

<222> (7) .. (12)

<220>

<221> UNSURE

<222> (14) .. (20)

<220>

<221> UNSURE

<222> (22) .. (28)

<220>

<221> UNSURE

<222> (30) .. (34)

<220>

<221> UNSURE

<222> (37) .. (45)

<220>

<221> UNSURE

<222> (47) .. (52)

<220>

<223> Description of Artificial Sequence:consensus

<400> 73

Gly Xaa Gly Xaa Xaa Gly Xaa Xaa Xaa Ala Xaa Xaa Leu Xaa Xaa Xaa
 1 5 10 15

Xaa Xaa Xaa Xaa Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa Glu Xaa Xaa Xaa
 20 25 30

Xaa Xaa Gly Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gly Xaa Xaa
 35 40 45

Xaa Xaa Xaa Xaa Gly
 50

<210> 74

<211> 43

<212> PRT

<213> Homo sapiens

<400> 74

Ser Glu Ala Tyr Ser Ala Lys Ile Ala Leu Phe Gly Ala Gly Pro Ala
 1 5 10 15

Ser Ile Ser Cys Ala Ser Phe Leu Ala Arg Leu Gly Tyr Ser Asp Ile
 20 25 30

Thr Ile Phe Glu Lys Gln Glu Tyr Val Gly Gly
 35 40

<210> 75

<211> 41

<212> PRT

<213> Agrobacterium vitis

<400> 75

Lys Val Ala Ile Val Gly Ala Gly Leu Ser Gly Leu Val Val Ala Ser
 1 5 10 15

Glu Leu Leu His Ala Gly Ile Asp Asp Val Thr Leu Tyr Glu Ala Ser
 20 25 30

Asp Arg Ile Gly Gly Lys Leu Trp Ser
 35 40

<210> 76
 <211> 45
 <212> PRT
 <213> *Deinococcus radiodurans*

<400> 76
 Val Lys Thr Gly Lys Lys Val Ala Val Val Gly Ser Gly Pro Ala Gly
 1 5 10 15
 Leu Ala Ala Ala Gln Gln Leu Ala Arg Ala Gly His Asp Val Thr Val
 20 25 30
 Phe Glu Lys Asn Asp Arg Val Gly Gly Arg Ile Glu Gln
 35 40 45

<210> 77
 <211> 37
 <212> PRT
 <213> *Arthrobacter nicotinovorans*

<400> 77
 Val Val Gly Gly Gly Phe Ser Gly Leu Lys Ala Ala Arg Asp Leu Thr
 1 5 10 15
 Asn Ala Gly Lys Lys Val Leu Leu Leu Glu Gly Gly Glu Arg Leu Gly
 20 25 30
 Gly Arg Ala Tyr Ser
 35

<210> 78
 <211> 52
 <212> PRT
 <213> *Synechocystis* sp.

<400> 78
 Arg Ile Ala Ile Ile Gly Ala Gly Leu Ala Gly Met Ala Thr Ala Val
 1 5 10 15
 Glu Leu Val Asp Ala Gly His Glu Val Glu Leu Tyr Glu Ala Arg Ser
 20 25 30
 Phe Ile Gly Gly Lys Val Gly Ser Trp Val Asp Gly Asp Gly Asn His
 35 40 45
 Ile Glu Met Gly

50

<210> 79

<211> 57

<212> PRT

<213> Cercospora nicotianae

<400> 79

Ser Thr Ser Lys Arg Pro Thr Ala Ile Val Ile Gly Ser Gly Val Gly
1 5 10 15

Gly Val Ser Thr Ala Ala Arg Leu Ala Arg Ala Gly Phe His Val Thr
20 25 30

Val Leu Glu Lys Asn Asn Phe Thr Gly Gly Arg Cys Ser Leu Ile His
35 40 45

His Glu Gly Tyr Arg Phe Asp Gln Gly
50 55

<210> 80

<211> 52

<212> PRT

<213> Zea mays

<400> 80

Arg Val Ile Val Val Gly Ala Gly Met Ser Gly Ile Ser Ala Ala Lys
1 5 10 15

Arg Leu Ser Glu Ala Gly Ile Thr Asp Leu Leu Ile Leu Glu Ala Thr
20 25 30

Asp His Ile Gly Gly Arg Met His Lys Thr Asn Phe Ala Gly Ile Asn
35 40 45

Val Glu Leu Gly
50

<210> 81

<211> 22

<212> DNA

<213> Propionibacterium acnes

<400> 81

ctatctcgag cacgaagaac gg

22

<210> 82

<211> 29

<212> DNA

<213> Propionibacterium acnes

<400> 82

ctattgatca tcacacgaag aaccgcgtc

29